/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 83.6%; Score 265.8; DB 14; Length 799;
Best Local Similarity 89.9%; Pred. No. 1.2e-69;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
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Db        101 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 160

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              |||||||| ||| ||| ||||| |||||||||||||||||||||| ||||| ||||| |
Db        161 GCCGGGCAAGTCGGAGCATTAGTACCTATTTAAATTGGTATCAGCATAAACCAGGGAAAG 220

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
              |||||||||||||||||| | |||||||| |||||||||||||||||||||| |||||||
Db        221 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 280

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||| |
Db        281 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 340

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||| ||||    | || |||||||  |||||||
Db        341 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAGACGTTCGGCCAAGGGACCA 400

Qy        302 AACTGGAGATCAAACGA 318
              |  ||||  ||||||||
Db        401 AGGTGGAAGTCAAACGA 417
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RESULT 12
CB985931
LOCUS CB985931 819 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13640497 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30328622 5', mRNA sequence.
ACCESSION CB985931
VERSION CB985931.1 GI:30280455
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM139 row: i column: 15
High quality sequence stop: 499.

FEATURES Location/Qualifiers
source 1. .819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30328622"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 83.6%; Score 265.8; DB 14; Length 819;
Best Local Similarity 89.9%; Pred. No. 1.2e-69;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
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Db        104 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGCGACAGAGTCACCATCACTT 163

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              |||||||| |||||||| ||||||||||||||||||||||||||||||||||||| |||||
Db        164 GCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAG 223

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
              ||||||| |||||||||| | |||||||| |||||||||||||||||||| |||||||
Db        224 CCCCTAACCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 283

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| |||||||||||||||||| |||||||||||||| |
Db        284 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 343

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||| |||    || |||||||  ||||||
Db        344 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGGACGTTCGGCCAATGGACCA 403

Qy        302 AACTGGAGATCAAACGA 318
              |  |||| |||||||||
Db        404 AGGTGGAAATCAAACGA 420
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RESULT 13
BG548281
LOCUS BG548281 864 bp mRNA linear EST 04-APR-2001
DEFINITION 602575248F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703483 5', mRNA sequence.
ACCESSION BG548281
VERSION BG548281.1 GI:13546946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 864)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1541  row: p  column: 12
           High quality sequence stop: 726.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4703483"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             83.6%;  Score 265.8;  DB 12;  Length 864;
  Best Local Similarity   89.9%;  Pred. No. 1.3e-69;
  Matches  285;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
              || | ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        100 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 159

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              |||||||| |||| || ||||||| |||||||||||||||||||||||| ||||| |
Db        160 GCCGGGCAAGTCACAGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAG 219

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
              |||||||| |||||||| | ||||||||| |||||||||||||||||||| |||||||
Db        220 CCCCTAAGATCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 279

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              ||||||||||||||||||||| |||||||||||||||||| |||||||||||||| |
Db        280 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 339

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||||||        || ||||||   |||||||
Db        340 TTGCAACTTACTACTGTCAACAGAGTTACACTACACCGCTCACTTTCGGCGGAGGGACCA 399

Qy        302 AACTGGAGATCAAACGA 318
                |||||||||||||||
Db        400 CGGTGGAGATCAAACGA 416


RESULT 14
BQ899146
LOCUS       BQ899146                 933 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8585624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302530
            5', mRNA sequence.
ACCESSION   BQ899146
VERSION     BQ899146.1  GI:22291160
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2520  row: c  column: 11
           High quality sequence start: 9
           High quality sequence stop: 589.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6302530"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             83.6%;  Score 265.8;  DB 13;  Length 933;
  Best Local Similarity   89.9%;  Pred. No. 1.3e-69;
  Matches  285;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
              || | ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        101 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 160

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              |||||||| |||||||||||||||||||| |||||||||||||||||||| | ||| |
Db        161 GCCGGGCAAGTCAGAGTATTAGCACCTTTTTAAATTGGTATCAGCAGAAACCAGCGAAAG 220

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
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Db        221 CCCCTACTCTCGTGATCTTTGCTGCATCCAATTTGCAAAGTGGGGTCCCATCAAGGTTCA 280

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| ||||||||||||||||  |||||||||||||| |
Db        281 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCCGTCTGCAACCTGAAGATT 340

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||||| ||||   |  || |||||||  |||||||
Db        341 TTGCAACTTACTACTGTCAACAGAGTTACATTACCCCCTGGACGTTCGGCCAAGGGACCA 400

Qy        302 AACTGGAGATCAAACGA 318
              |  |||| |||||||||
Db        401 AGGTGGAAATCAAACGA 417


RESULT 15
BQ708832
LOCUS       BQ708832                 992 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353479 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279561
            5', mRNA sequence.
ACCESSION   BQ708832
VERSION     BQ708832.1  GI:21847731
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 992)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: f  column: 10
            High quality sequence start: 5
            High quality sequence stop: 696.
FEATURES            Location/Qualifiers
     source         1. .992
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6279561"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_113"
                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed  by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of  California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
ORIGIN

  Query Match            83.6%;  Score 265.8;  DB 13;  Length 992;
  Best Local Similarity  89.9%;  Pred. No. 1.4e-69;
  Matches  285;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
              || | |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        105 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 164

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
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Db        165 GCCGGGCAAGTCAGAGTATTAGCACCTTTTTAAATTGGTATCAGCAGAAACCAGCGAAAG 224

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
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Db        225 CCCCTACTCTCGTGATCTTTGCTGCATCCAATTTGCAAAGTGGGGTCCCATCAAGGTTCA 284

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| |||||||||||||||||  |||||||||||||| |
Db        285 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCCGTCTGCAACCTGAAGATT 344

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||| ||||   |  || |||||||  |||||||
Db        345 TTGCAACTTACTACTGTCAACAGAGTTACATTACCCCCTGGACGTTCGGCCAAGGGACCA 404

Qy        302 AACTGGAGATCAAACGA 318
              |  |||| |||||||||
Db        405 AGGTGGAAATCAAACGA 421


Search completed: August 13, 2004, 07:13:24
Job time : 1865.96 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 207.182 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcacccagtctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	316.4	99.5	318	6	ABK89641	Abk89641 DNA encod
2	276.4	86.9	321	5	AAH68647	Aah68647 Human ant
3	276.4	86.9	321	5	AAH68701	Aah68701 Human ant
4	276.4	86.9	321	8	ACD45311	Acd45311 Anti-Rh(D
5	276.4	86.9	321	8	ACD45365	Acd45365 Anti-Rh(D
6	273.4	86.0	315	2	AAV19761	Aav19761 Antibody
7	273.2	85.9	321	5	AAH68720	Aah68720 Human ant
8	273.2	85.9	321	5	AAH68658	Aah68658 Human ant
9	273.2	85.9	321	5	AAH68652	Aah68652 Human ant
10	273.2	85.9	321	5	AAH68713	Aah68713 Human ant
11	273.2	85.9	321	5	AAH68703	Aah68703 Human ant
12	273.2	85.9	321	8	ACD45377	Acd45377 Anti-Rh(D
13	273.2	85.9	321	8	ACD45367	Acd45367 Anti-Rh(D
14	273.2	85.9	321	8	ACD45384	Acd45384 Anti-Rh(D
15	273.2	85.9	321	8	ACD45316	Acd45316 Anti-Rh(D
16	273.2	85.9	321	8	ACD45322	Acd45322 Anti-Rh(D
17	271.6	85.4	321	5	AAH68723	Aah68723 Human ant
18	271.6	85.4	321	5	AAH68651	Aah68651 Human ant
19	271.6	85.4	321	5	AAH68724	Aah68724 Human ant
20	271.6	85.4	321	5	AAH68707	Aah68707 Human ant
21	271.6	85.4	321	8	ACD45371	Acd45371 Anti-Rh(D
22	271.6	85.4	321	8	ACD45388	Acd45388 Anti-Rh(D
23	271.6	85.4	321	8	ACD45387	Acd45387 Anti-Rh(D
24	271.6	85.4	321	8	ACD45315	Acd45315 Anti-Rh(D
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26	271.2	85.3	720	7	ABZ76706	Abz76706 Human ser
27	270.6	85.1	396	2	AAT75423	Aat75423 Human ant
28	270	84.9	321	5	AAH68717	Aah68717 Human ant
29	270	84.9	321	5	AAH68719	Aah68719 Human ant
30	270	84.9	321	8	ACD45383	Acd45383 Anti-Rh(D
31	270	84.9	321	8	ACD45381	Acd45381 Anti-Rh(D
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33	269	84.6	729	6	ABL46009	Abl46009 Humanised
34	268.4	84.4	321	5	AAH68650	Aah68650 Human ant
35	268.4	84.4	321	8	ACD45314	Acd45314 Anti-Rh(D
36	268.4	84.4	342	4	AAH47727	Aah47727 Nucleotid
37	268	84.3	324	7	AAL52122	Aal52122 Human ant
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39	268	84.3	333	5	AAH74684	Aah74684 Nucleotid
40	268	84.3	333	7	ABT34320	Abt34320 Hepatitis
41	268	84.3	900	5	AAH74688	Aah74688 Nucleotid
42	268	84.3	900	7	ABT34324	Abt34324 Hepatitis
43	267.4	84.1	324	4	AAF29073	Aaf29073 Human HIV
44	267.4	84.1	333	5	AAH74685	Aah74685 Nucleotid
45	267.4	84.1	333	7	ABT34321	Abt34321 Hepatitis

ALIGNMENTS

RESULT 1
ABK89641
ID ABK89641 standard; DNA; 318 BP.
XX
AC ABK89641;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 60 light chain.
XX
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .318
FT /*tag= a
FT /product= "Fab clone 60 heavy chain"
FT /transl_except= (pos:292. .294, aa:Ser)
FT misc_feature 7. .63
FT /*tag= b
FT /note= "FR1 region"
FT misc_feature 64. .96
FT /*tag= c
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FT misc_feature 97. .141
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FT /*tag= e
FT /note= "CDR2 region"
FT misc_feature 163. .258
FT /*tag= f
FT /note= "FR3 region"
FT misc_feature 259. .285
FT /*tag= g
FT /note= "CDR3 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.

```
XX
PA   (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI   Flicker S,  Steinberger P,  Kraft D,  Valenta R;
XX
DR   WPI; 2002-583604/62.
DR   P-PSDB; ABG30449.
XX
PT   Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT   variable region of group 2 allergen specific-human IgE Fabs, useful for
PT   diagnosing or passive immunotherapy of type I allergy, for environmental
PT   allergen detection.
XX
PS   Disclosure; Page 35; 45pp; English.
XX
CC   This invention relates to the DNA and protein sequences of group 2
CC   allergen-specific human IgE Fabs and methods for their use. The proteins
CC   of the invention may have antiallergic activities and may be used as a
CC   vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC   antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC   2 allergen-specific fabs of the invention may be useful for environmental
CC   allergen detection and for standardisation of allergen extracts. The fabs
CC   - or a vaccine againts a type I allergy is useful for passive
CC   immunotherapy of type I allergy, it is also useful for diagnosing a type
CC   I allergy. The allergen-specific fabs of the invention are useful for
CC   inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC   also useful for identification of group 2 allergen-containing pollen and
CC   may be used for blocking the binding of grass pollen allergic patients
CC   IgE antibodies to PhI p 2. The present sequence represents the DNA
CC   encoding the human IgG fab, clone 60 light chain protein of the invention
XX
SQ   Sequence 318 BP; 83 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

  Query Match            99.5%;  Score 316.4;  DB 6;  Length 318;
  Best Local Similarity  99.7%;  Pred. No. 9.7e-92;
  Matches  317;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCTAAGCTCCTGATCTGGAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300

Qy        301 AAACTGGAGATCAAACGA 318
              ||||||||||||||||||
Db        301 AAACTGGAGATCAAACGA 318


RESULT 2
AAH68647
ID   AAH68647 standard; DNA; 321 BP.
XX
AC   AAH68647;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) chain I02 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93590.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 2; Col 54; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

  Query Match            86.9%;  Score 276.4;  DB 5;  Length 321;
  Best Local Similarity  91.8%;  Pred. No. 7.7e-79;
  Matches  292;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              |||||||| ||||||| ||||||| |||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| | |  || ||||||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 3
AAH68701
ID   AAH68701 standard; DNA; 321 BP.
```

XX
AC AAH68701;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH13 nucleotide sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR P-PSDB; AAG93644.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Example 3; Col 74; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 86.9%; Score 276.4; DB 5; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.7e-79;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | ||||||| ||||| |||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||| |||| || || || |||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              || ||||||||||||||||
Db        304 AAGCTGGAGATCAAACGA 321
```

RESULT 4
ACD45311
ID ACD45311 standard; DNA; 321 BP.
XX
AC ACD45311;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) chain I02 DNA.
XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR P-PSDB; ABO27397.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 12; Page 39; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 86.9%; Score 276.4; DB 8; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.7e-79;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | ||||||| ||||| |||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||| |||| | |  || ||||||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303
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Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 5
ACD45365
ID   ACD45365 standard; DNA; 321 BP.
XX
AC   ACD45365;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) light chain SH13 DNA.
XX
KW   Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW   magnetically activated cell sorting.
XX
OS   Homo sapiens.
XX
PN   US2003040605-A1.
XX
PD   27-FEB-2003.
XX
PF   04-MAY-2001; 2001US-00848798.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
PR   29-JAN-1999;   99US-00240274.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2003-512273/48.
DR   P-PSDB; ABO27451.
XX
PT   New human Rh(D)-binding protein useful for various diagnostic and
PT   therapeutic applications, including typing of blood or blood products.
XX
PS   Claim 12; Page 57; 187pp; English.
XX
CC   The invention relates to an isolated Rh(D) binding protein. The protein
CC   can be used for magnetically activated cell sorting. The protein is
CC   useful in various diagnostic and therapeutic applications in humans,
CC   including typing of blood or blood products. The present sequence
CC   represents DNA encoding a human anti-Rh(D) chain
XX
SQ   Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

  Query Match             86.9%;  Score 276.4;  DB 8;  Length 321;
  Best Local Similarity   91.8%;  Pred. No. 7.7e-79;
  Matches  292;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | |||||||| ||||| |||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||||| ||||   || || || ||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              || ||||||||||||||
Db        304 AAGCTGGAGATCAAACGA 321


RESULT 6
AAV19761
ID   AAV19761 standard; DNA; 315 BP.
XX
AC   AAV19761;
XX
DT   12-JUN-1998  (first entry)
XX
DE   Antibody LD2-20-VL chain coding sequence.
XX
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9749809-A1.
XX
PD   31-DEC-1997.
XX
PF   20-JUN-1997;   97WO-EP003253.
XX
PR   24-JUN-1996;   96EP-00810421.
XX
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI   Miescher S,  Vogel M,  Stadler B,  Morell A,  Imboden M,  Amstutz H;
XX
DR   WPI; 1998-077173/07.
DR   P-PSDB; AAW52237.
XX
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise Rhesus
PT   D antigen in therapy, e.g. for treating idiopathic thrombocytopenic
PT   purpura.
XX
PS   Claim 6; Fig 13B; 68pp; English.
XX
CC   This sequence encodes the antibody LD2-20-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative women before or immediately after the birth
CC   of a Rhesus positive child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents
XX
SQ   Sequence 315 BP; 84 A; 83 C; 71 G; 77 T; 0 U; 0 Other;

  Query Match             86.0%;  Score 273.4;  DB 2;  Length 315;
  Best Local Similarity   91.7%;  Pred. No. 7.1e-78;
  Matches  289;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              | | | ||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          1 GTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 60

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
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                ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db          61 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 120

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
                |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db         121 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 180

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
                |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db         181 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 240

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
                ||||||| |||||||||||||||||||||| ||||  ||  || ||||||||||||||||
Db         241 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCGATTCACTTTCGGCCCTGGGACC 300

Qy         301 AAACTGGAGATCAAA 315
                ||| |||| ||||||
Db         301 AAAGTGGATATCAAA 315


RESULT 7
AAH68720
ID   AAH68720 standard; DNA; 321 BP.
XX
AC   AAH68720;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) antibody clone SH49 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93663.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 3; Col 79; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 273.2;  DB 5;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy           1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
               |||||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Db           4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCACT 63

Qy          61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
               |||||||| ||||||| ||||||| |||||||||||||||||||||||||||| |||||
Db          64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
               |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db         124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
               ||||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||
Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
               ||||||| |||||||||||||||||||| ||||  |  || ||||||| ||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
               ||  |||| |||||||||
Db         304 AAGGTGGAAATCAAACGA 321


RESULT 8
AAH68658
ID   AAH68658 standard; DNA; 321 BP.
XX
AC   AAH68658;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) chain I13 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93601.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 2; Col 57; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
```

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CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 82 A; 88 C; 77 G; 74 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 273.2;  DB 5;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| |||||||  ||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | ||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              |||||||  |||||||||||||||||||||  ||||    | |  ||  ||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCTCACAGTTTTGGCCGGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGCTGGAGATCAAACGA 321


RESULT 9
AAH68652
ID   AAH68652 standard; DNA; 321 BP.
XX
AC   AAH68652;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) chain I07 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93595.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 2; Col 55; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 273.2;  DB 5;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| |||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | ||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              |||||||  |||||||||||||||||||||  ||||       || ||||||   ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGGTGGAGATCAAACGA 321


RESULT 10
AAH68713
ID   AAH68713 standard; DNA; 321 BP.
XX
AC   AAH68713;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) antibody clone SH36 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
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DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93656.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 3; Col 77; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 273.2;  DB 5;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||  ||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db          4 GAGCTCACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              |||||||| |||||||  |||||||  ||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||  |||||||||||||||||||||| ||||||
Db        124 TCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||||| ||||||||||||||||||  ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              |||||||  ||||||||||||||||||||||| ||||    | ||||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              |||  ||||  |||||||||
Db        304 AAAGTGGATATCAAACGA 321


RESULT 11
AAH68703
ID   AAH68703 standard; DNA; 321 BP.
XX
AC   AAH68703;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) antibody clone SH16 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93646.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 3; Col 75; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 273.2;  DB 5;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              |||||||| |||||||  |||||||  ||||||||||||||||| ||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||  |||||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||||| ||||||||||||||||||  ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              |||||||  ||||||||||||||||||||||| ||||      || ||||||   ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGGTGGAGATCAAACGA 321


RESULT 12
ACD45377
ID   ACD45377 standard; DNA; 321 BP.
XX
AC   ACD45377;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) light chain SH36 DNA.
XX
KW   Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW   magnetically activated cell sorting.
XX
```

```
OS   Homo sapiens.
XX
PN   US2003040605-A1.
XX
PD   27-FEB-2003.
XX
PF   04-MAY-2001; 2001US-00848798.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
PR   29-JAN-1999;   99US-00240274.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2003-512273/48.
DR   P-PSDB; ABO27463.
XX
PT   New human Rh(D)-binding protein useful for various diagnostic and
PT   therapeutic applications, including typing of blood or blood products.
XX
PS   Claim 12; Page 60; 187pp; English.
XX
CC   The invention relates to an isolated Rh(D) binding protein. The protein
CC   can be used for magnetically activated cell sorting. The protein is
CC   useful in various diagnostic and therapeutic applications in humans,
CC   including typing of blood or blood products. The present sequence
CC   represents DNA encoding a human anti-Rh(D) chain
XX
SQ   Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;

  Query Match            85.9%;  Score 273.2;  DB 8;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||| |||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              |||||||| ||||||| ||||||| |||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||| | |||||||| |||||||||||||||||||| ||||||
Db        124 TCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||| ||||      | ||||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAAGTGGATATCAAACGA 321


RESULT 13
ACD45367
ID   ACD45367 standard; DNA; 321 BP.
XX
AC   ACD45367;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) light chain SH16 DNA.
XX
KW   Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW   magnetically activated cell sorting.
XX
OS   Homo sapiens.
XX
PN   US2003040605-A1.
XX
PD   27-FEB-2003.
XX
PF   04-MAY-2001; 2001US-00848798.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
PR   29-JAN-1999;   99US-00240274.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2003-512273/48.
DR   P-PSDB; ABO27453.
XX
PT   New human Rh(D)-binding protein useful for various diagnostic and
PT   therapeutic applications, including typing of blood or blood products.
XX
PS   Claim 12; Page 57; 187pp; English.
XX
CC   The invention relates to an isolated Rh(D) binding protein. The protein
CC   can be used for magnetically activated cell sorting. The protein is
CC   useful in various diagnostic and therapeutic applications in humans,
CC   including typing of blood or blood products. The present sequence
CC   represents DNA encoding a human anti-Rh(D) chain
XX
SQ   Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;

  Query Match            85.9%;  Score 273.2;  DB 8;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 8.3e-78;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              |||||||| |||||||| ||||||| ||||||||||||||||| |||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||| ||||      || ||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGGTGGAGATCAAACGA 321


RESULT 14
ACD45384
ID   ACD45384 standard; DNA; 321 BP.
XX
AC   ACD45384;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) light chain SH49 DNA.
```

XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR P-PSDB; ABO27470.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 12; Page 61; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 85.9%; Score 273.2; DB 8; Length 321;
Best Local Similarity 91.2%; Pred. No. 8.3e-78;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```
Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
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Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
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Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGGTGGAAATCAAACGA 321
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RESULT 15
ACD45316
ID ACD45316 standard; DNA; 321 BP.
XX
AC ACD45316;
XX
DT 12-SEP-2003 (first entry)

XX
DE Anti-Rh(D) chain I07 DNA.
XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR P-PSDB; ABO27402.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 12; Page 40; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 85.9%; Score 273.2; DB 8; Length 321;
Best Local Similarity 91.2%; Pred. No. 8.3e-78;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
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Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGGTGGAGATCAAACGA 321
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Search completed: August 13, 2004, 01:35:53
Job time : 208.182 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 706.827 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcacccagtctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	318	100.0	318	15	US-10-027-725A-5	Sequence 5, Appli
2	276.4	86.9	321	10	US-09-848-798-102	Sequence 102, App
3	276.4	86.9	321	10	US-09-848-798-199	Sequence 199, App
4	273.2	85.9	321	10	US-09-848-798-107	Sequence 107, App
5	273.2	85.9	321	10	US-09-848-798-113	Sequence 113, App
6	273.2	85.9	321	10	US-09-848-798-201	Sequence 201, App
7	273.2	85.9	321	10	US-09-848-798-211	Sequence 211, App
8	273.2	85.9	321	10	US-09-848-798-218	Sequence 218, App
9	272.2	85.6	384	16	US-10-309-762-115	Sequence 115, App
10	271.6	85.4	321	10	US-09-848-798-106	Sequence 106, App
11	271.6	85.4	321	10	US-09-848-798-205	Sequence 205, App
12	271.6	85.4	321	10	US-09-848-798-221	Sequence 221, App
13	271.6	85.4	321	10	US-09-848-798-222	Sequence 222, App
14	271.2	85.3	720	9	US-09-192-854-1	Sequence 1, Appli
15	271.2	85.3	720	9	US-09-968-561A-1	Sequence 1, Appli
16	271.2	85.3	720	10	US-09-968-744A-1	Sequence 1, Appli
17	271.2	85.3	720	13	US-09-968-561A-1	Sequence 1, Appli
18	270	84.9	321	10	US-09-848-798-215	Sequence 215, App
19	270	84.9	321	10	US-09-848-798-217	Sequence 217, App
20	269.2	84.7	321	17	US-10-663-244-78	Sequence 78, Appl
21	269	84.6	729	15	US-10-216-484-125	Sequence 125, App
22	269	84.6	729	15	US-10-384-933-125	Sequence 125, App
23	268.4	84.4	321	10	US-09-848-798-105	Sequence 105, App
24	268	84.3	324	17	US-10-344-514-3	Sequence 3, Appli
25	268	84.3	324	17	US-10-344-514-4	Sequence 4, Appli
26	268	84.3	324	17	US-10-344-514-7	Sequence 7, Appli
27	268	84.3	324	17	US-10-344-514-8	Sequence 8, Appli
28	268	84.3	333	15	US-10-203-754A-60	Sequence 60, Appl
29	268	84.3	900	15	US-10-203-754A-64	Sequence 64, Appl
30	267.4	84.1	333	15	US-10-203-754A-61	Sequence 61, Appl
31	267.4	84.1	714	15	US-10-153-382-18	Sequence 18, Appl
32	267.4	84.1	900	15	US-10-203-754A-65	Sequence 65, Appl
33	267	84.0	322	17	US-10-038-591-54	Sequence 54, Appl
34	265.2	83.4	321	10	US-09-848-798-109	Sequence 109, App
35	265.2	83.4	321	10	US-09-848-798-216	Sequence 216, App
36	263.8	83.0	322	16	US-10-309-762-226	Sequence 226, App
37	263.8	83.0	322	16	US-10-309-762-227	Sequence 227, App
38	263.6	82.9	318	15	US-10-027-725A-4	Sequence 4, Appli
39	263.6	82.9	321	10	US-09-848-798-207	Sequence 207, App
40	263.4	82.8	324	10	US-09-848-798-101	Sequence 101, App
41	263.4	82.8	324	10	US-09-848-798-112	Sequence 112, App
42	263.4	82.8	324	10	US-09-848-798-210	Sequence 210, App
43	262.2	82.5	322	16	US-10-309-762-221	Sequence 221, App
44	262.2	82.5	322	16	US-10-309-762-233	Sequence 233, App
45	262	82.4	321	10	US-09-848-798-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-10-027-725A-5
; Sequence 5, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-5

Query Match 100.0%; Score 318; DB 15; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.1e-100;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Db        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300

Qy        301 AAACTGGAGATCAAACGA 318
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Db        301 AAACTGGAGATCAAACGA 318


RESULT 2
US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-848-798-102

  Query Match             86.9%;  Score 276.4;  DB 10;  Length 321;
  Best Local Similarity   91.8%;  Pred. No. 2e-85;
  Matches  292;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
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Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGGTGGAAATCAAACGA 321


RESULT 3
US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199

  Query Match             86.9%;  Score 276.4;  DB 10;  Length 321;
  Best Local Similarity   91.8%;  Pred. No. 2e-85;
  Matches  292;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | ||||||||| ||||| ||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGCTGGAGATCAAACGA 321


RESULT 4
US-09-848-798-107
; Sequence 107, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-798-107

  Query Match             85.9%;  Score 273.2;  DB 10;  Length 321;
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  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
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Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| || ||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGGTGGAGATCAAACGA 321


RESULT 5
US-09-848-798-113
; Sequence 113, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I13
US-09-848-798-113

  Query Match             85.9%;  Score 273.2;  DB 10;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||||| | ||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| || ||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCTCACAGTTTTGGCCGGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGCTGGAGATCAAACGA 321


RESULT 6
US-09-848-798-201
; Sequence 201, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-848-798-201

  Query Match             85.9%;  Score 273.2;  DB 10;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||||| | ||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| || ||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  ||||||||||||||
Db        304 AAGGTGGAGATCAAACGA 321


RESULT 7
US-09-848-798-211
; Sequence 211, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
```

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;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-848-798-211

  Query Match            85.9%;  Score 273.2;  DB 10;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          4 GAGCTCACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 TCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||       | ||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAAGTGGATATCAAACGA 321


RESULT 8
US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218

  Query Match            85.9%;  Score 273.2;  DB 10;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 9
US-10-309-762-115
; Sequence 115, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
;   LENGTH: 384
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-115

  Query Match            85.6%;  Score 272.2;  DB 16;  Length 384;
  Best Local Similarity   91.2%;  Pred. No. 6.3e-84;
  Matches  289;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
              || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db         68 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACCATCACTT 127

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              |||||||| ||||||| ||||||| |||||||||||||||||| |||||||| ||||| |
Db        128 GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
              |||||||||||||||||| || |||||||||||||| | |||||||||||||| |||||||
Db        188 CCCCTAAGCTCCTGATCTATACTGCATCCAATTTGCGAGGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| |||||||||||||||||  |||||||||||||| |
Db        248 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCTGAAGATT 307

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||| | || |||  || ||||||||||||||||
Db        308 TTGCAACTTACTACTGTCAACAGAGTTACAGTTCCCTATTCACTTTCGGCCCTGGGACCA 367
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Qy        302 AACTGGAGATCAAACGA 318
              || |||| |||||||||
Db        368 AAGTGGATATCAAACGA 384


RESULT 10
US-09-848-798-106
; Sequence 106, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-106

  Query Match             85.4%;  Score 271.6;  DB 10;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.5e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |   ||||||| ||||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||      |||||||||  |||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGACA 303

Qy        301 AAACTGGAGATCAAACGA 318
                |||||||||  ||||||
Db        304 CGACTGGAGATTAAACGA 321


RESULT 11
US-09-848-798-205
; Sequence 205, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-09-848-798-205

  Query Match             85.4%;  Score 271.6;  DB 10;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.5e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| |||||||||||||||||||||||||||| ||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAGACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||| |||||||||| |  |||||||| |||||||| |||||||||| ||||||
Db        124 GCCCCTAACCTCCTGATCTATGCTGCATCCACTTTGCAAAGGGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              | |||||||||||||||||| |||||||||||||||| |||||||||||||||
Db        184 ACTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||||| | |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACACTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||| ||||
Db        304 AAGATGGAAATCAGACGA 321


RESULT 12
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

  Query Match             85.4%;  Score 271.6;  DB 10;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.5e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||||||||||||||||||| ||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63
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Qy          61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
               ||||||||| ||||||| ||| |||| |||||||||||||||||||||||||| |||||
Db          64 TGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
               |||||||||||||||||| |  |||||||| |||||||||||||||||| ||||||
Db         124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
               |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
               ||||||| |||||||||||||||||||||||| ||||   |  || |||||||  ||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
               ||  |||| |||||||||
Db         304 AAGGTGGAAATCAAACGA 321


RESULT 13
US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

  Query Match             85.4%;  Score 271.6;  DB 10;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.5e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy           1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
               |||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Db           4 GAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy          61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
               ||||||||| ||||||| ||| |||| |||||||||||||||||||||||||| |||||
Db          64 TGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
               |||||||||||||||||| |  |||||||| |||||||||||||||||| ||||||
Db         124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
               |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
               ||||||| |||||||||||||||||||||||| ||||   |  || |||||||  ||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
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Db         304 AAGGTGGAAATCAAACGA 321


RESULT 14
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-192-854-1

  Query Match             85.3%;  Score 271.2;  DB 9;  Length 720;
  Best Local Similarity   91.1%;  Pred. No. 1.8e-83;
  Matches  288;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy           2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
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Db         404 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 463

Qy          62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
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Db         464 GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAG 523

Qy         122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
               |||||||||||||||||| |  |||||||| |||||||||||||||||||| |||||||
Db         524 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 583

Qy         182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
               |||||||||||||||||||||| |||||||||||||||||||||||||||||||||| |
Db         584 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 643

Qy         242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
               |||||| |||||||||||||||||||||| ||||    |||| |||||||  |||||||
Db         644 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAAGGGACCA 703

Qy         302 AACTGGAGATCAAACG 317
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Db         704 AGGTGGAAATCAAACG 719


RESULT 15
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
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;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-561A-1

  Query Match             85.3%;  Score 271.2;  DB 9;  Length 720;
  Best Local Similarity   91.1%;  Pred. No. 1.8e-83;
  Matches  288;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACTT 61
              || | |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        404 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 463

Qy         62 GCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAGG 121
              ||||||| ||||||| ||||||| ||||||||||||||||||||||||| ||||| |
Db        464 GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAG 523

Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
              |||||||||||||||| |  |||||||| |||||||||||||||||||| |||||||
Db        524 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 583

Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
              |||||||||||||||||||| |||||||||||||||| |||||||||||||| |
Db        584 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 643

Qy        242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
              |||||| |||||||||||||||||||||| ||||    |||| |||||||  |||||||
Db        644 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAAGGGACCA 703

Qy        302 AACTGGAGATCAAACG 317
              |  |||| ||||||||
Db        704 AGGTGGAAATCAAACG 719


Search completed: August 13, 2004, 19:18:24
Job time : 707.827 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 44.9697 Seconds
(without alignments)
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Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcacccagtctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	276.4	86.9	321	3	US-09-240-274-102	Sequence 102, App
2	276.4	86.9	321	3	US-09-240-274-199	Sequence 199, App
3	273.2	85.9	321	3	US-09-240-274-107	Sequence 107, App
4	273.2	85.9	321	3	US-09-240-274-113	Sequence 113, App
5	273.2	85.9	321	3	US-09-240-274-201	Sequence 201, App
6	273.2	85.9	321	3	US-09-240-274-211	Sequence 211, App
7	273.2	85.9	321	3	US-09-240-274-218	Sequence 218, App
8	271.6	85.4	321	3	US-09-240-274-106	Sequence 106, App
9	271.6	85.4	321	3	US-09-240-274-205	Sequence 205, App
10	271.6	85.4	321	3	US-09-240-274-221	Sequence 221, App
11	271.6	85.4	321	3	US-09-240-274-222	Sequence 222, App
12	270	84.9	321	3	US-09-240-274-215	Sequence 215, App
13	270	84.9	321	3	US-09-240-274-217	Sequence 217, App
14	268.4	84.4	321	3	US-09-240-274-105	Sequence 105, App
15	267.4	84.1	714	4	US-09-472-087-62	Sequence 62, Appl
16	265.2	83.4	321	3	US-09-240-274-109	Sequence 109, App
17	265.2	83.4	321	3	US-09-240-274-216	Sequence 216, App
18	263.6	82.9	321	3	US-09-240-274-207	Sequence 207, App
19	263.4	82.8	324	3	US-09-240-274-101	Sequence 101, App
20	263.4	82.8	324	3	US-09-240-274-112	Sequence 112, App
21	263.4	82.8	324	3	US-09-240-274-210	Sequence 210, App
22	262.4	82.5	451	4	US-09-472-087-50	Sequence 50, Appl
23	262	82.4	321	3	US-09-240-274-104	Sequence 104, App
24	261.8	82.3	324	3	US-09-240-274-110	Sequence 110, App
25	261.8	82.3	324	3	US-09-240-274-206	Sequence 206, App
26	261.4	82.2	402	4	US-09-472-087-49	Sequence 49, Appl
27	261.2	82.1	321	2	US-08-378-939-13	Sequence 13, Appl
28	260.4	81.9	321	3	US-09-240-274-103	Sequence 103, App
29	260	81.8	672	4	US-09-456-090A-47	Sequence 47, Appl
30	256.6	80.7	417	4	US-09-472-087-48	Sequence 48, Appl
31	256.2	80.6	458	4	US-09-472-087-44	Sequence 44, Appl
32	255.4	80.3	324	3	US-09-240-274-224	Sequence 224, App
33	254	79.9	321	3	US-09-240-274-200	Sequence 200, App
34	254	79.9	321	3	US-09-240-274-213	Sequence 213, App
35	252.4	79.4	318	3	US-09-240-274-202	Sequence 202, App
36	250.8	78.9	318	3	US-09-240-274-208	Sequence 208, App
37	250.8	78.9	321	3	US-09-240-274-108	Sequence 108, App
38	250.8	78.9	321	3	US-09-240-274-114	Sequence 114, App
39	250.8	78.9	321	3	US-09-240-274-203	Sequence 203, App
40	247.2	77.7	705	1	US-08-488-376-16	Sequence 16, Appl
41	247.2	77.7	705	2	US-08-634-223-16	Sequence 16, Appl
42	247.2	77.7	705	2	US-08-634-224-16	Sequence 16, Appl
43	247.2	77.7	705	2	US-08-634-400-16	Sequence 16, Appl
44	247.2	77.7	705	2	US-08-635-878-16	Sequence 16, Appl
45	247.2	77.7	705	2	US-08-770-057-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match 86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 2e-85;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
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Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| | |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||| |||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| |||| | |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGGTGGAAATCAAACGA 321


RESULT 2
US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

  Query Match             86.9%;  Score 276.4;  DB 3;  Length 321;
  Best Local Similarity   91.8%;  Pred. No. 2e-85;
  Matches  292;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| ||||| ||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||    || || || ||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGCTGGAGATCAAACGA 321


RESULT 3
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

  Query Match             85.9%;  Score 273.2;  DB 3;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| ||||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| ||||| ||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||    || |||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTCGAACTTTCGGCGGAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
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Db        304 AAGGTGGAGATCAAACGA 321


RESULT 4
US-09-240-274-113
; Sequence 113, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I13
US-09-240-274-113

  Query Match             85.9%;  Score 273.2;  DB 3;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
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Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
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Db          64 TGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
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Db         124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
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Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
                ||||||| |||||||||||||||||||||||| ||||    | |  || ||||  ||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCTCACAGTTTTGGCCGGGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
                || ||||||||||||||
Db         304 AAGCTGGAGATCAAACGA 321


RESULT 5
US-09-240-274-201
; Sequence 201, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

  Query Match             85.9%;  Score 273.2;  DB 3;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy           1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy          61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
               ||||||||| ||||||| ||||||| |||||||||||||||||| |||||||| |||||
Db          64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
               |||||||||||||||||| | |||||||| ||||||||||||||||||||| ||||||
Db         124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
               |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
               ||||||| ||||||||||||||||||||||| ||||      || ||||||   ||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCAACTTTCGGCGGAGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
               ||  |||||||||||||
Db         304 AAGGTGGAGATCAAACGA 321


RESULT 6
US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

  Query Match             85.9%;  Score 273.2;  DB 3;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy           1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
               |||||||| ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db           4 GAGCTCACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy          61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
               ||||||||| ||||||| ||||||| |||||||||||||||||||||||||||| |||||
Db          64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy         121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
               |||||||||||||||||| | |||||||| ||||||||||||||||||||| ||||||
Db         124 TCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy         181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
               |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy         241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
               ||||||| |||||||||||||||||||||||| ||||      | ||||||||||||||
Db         244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGACC 303

Qy         301 AAACTGGAGATCAAACGA 318
               ||| |||| |||||||||
Db         304 AAAGTGGATATCAAACGA 321


RESULT 7
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
```

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;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

  Query Match             85.9%;  Score 273.2;  DB 3;  Length 321;
  Best Local Similarity   91.2%;  Pred. No. 2.6e-84;
  Matches  290;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||| ||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||||| ||||   |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 8
US-09-240-274-106
; Sequence 106, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I06
US-09-240-274-106

  Query Match             85.4%;  Score 271.6;  DB 3;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.1e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||||||| |||||||||||||||||||||||| ||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||||| |||||||||||||||||||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGACA 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||||||||| ||||||
Db        304 CGACTGGAGATTAAACGA 321


RESULT 9
US-09-240-274-205
; Sequence 205, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-09-240-274-205

  Query Match             85.4%;  Score 271.6;  DB 3;  Length 321;
  Best Local Similarity   90.9%;  Pred. No. 9.1e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| |||||||||||||||||||||||||||||||| ||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAGACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||| |||||||||| |  |||||||| |||||||| |||||||||||| ||||||
Db        124 GCCCCTAACCTCCTGATCTATGCTGCATCCACTTTGCAAAGGGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              | ||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Db        184 ACTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCCTGTGGACGTTCGGCCAAGGGACC 300
              ||||||| |||||||||||||||||||||||| | |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACACTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||| ||||
Db        304 AAGATGGAAATCAGACGA 321


RESULT 10
US-09-240-274-221
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; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

  Query Match            85.4%;  Score 271.6;  DB 3;  Length 321;
  Best Local Similarity  90.9%;  Pred. No. 9.1e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||| |||| ||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||  |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 11
US-09-240-274-222
; Sequence 222, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

  Query Match            85.4%;  Score 271.6;  DB 3;  Length 321;
  Best Local Similarity  90.9%;  Pred. No. 9.1e-84;
  Matches  289;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| ||||||| ||| |||| ||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||||||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||||||| ||||  |  || |||||||  ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||  |||| |||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 12
US-09-240-274-215
; Sequence 215, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 215
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH46
US-09-240-274-215

  Query Match            84.9%;  Score 270;  DB 3;  Length 321;
  Best Local Similarity  90.6%;  Pred. No. 3.2e-83;
  Matches  288;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| |||||   |||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGTACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              ||||||| |||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAATCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183
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Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||| ||||| | ||      || ||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGACTTACAGTTCCCCTAGCACTTTCGGCCCTGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAAGTGGATATCAAACGA 321
```

RESULT 13
US-09-240-274-217
; Sequence 217, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

Query Match 84.9%; Score 270; DB 3; Length 321;
Best Local Similarity 90.6%; Pred. No. 3.2e-83;
Matches 288; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

```
Qy          1 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCACT 60
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGCCGGGCACGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 120
              ||||||||| |||||   ||||||| |||||||||||||||||||||||||| |||||
Db         64 TGCCGGGCAAGTCAGTACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTC 180
              |||||||| |||||||||| |  |||||||| |||||||||||||||||||| ||||||
Db        124 GCCCCTAATCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
              |||||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
              ||||||| |||||||||||||||||| ||||| | ||      || ||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGACTTACAGTTCCCCTAGCACTTTCGGCCCTGGGACC 303

Qy        301 AAACTGGAGATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAAGTGGATATCAAACGA 321
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RESULT 14
US-09-240-274-105
; Sequence 105, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-105

Query Match 84.4%; Score 268.4; DB 3; Length 321;
Best Local Similarity 90.3%; Pred. No. 1.1e-82;
Matches 287; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Qy        241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Qy        301 AAACTGGAGATCAAACGA 318
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RESULT 15
US-09-472-087-62
; Sequence 62, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-472-087-62

Query Match 84.1%; Score 267.4; DB 4; Length 714;
Best Local Similarity 90.2%; Pred. No. 3.7e-82;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db         74 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

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Qy        122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAATTTGCAAAGTGGGGTCCCATCCAGGTTCA 181
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Qy        182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
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Job time : 45.9697 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1368.2 Seconds
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Title: US-10-027-725A-6
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	318	100.0	318	9	HSA458381	AJ458381 Homo sapi
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4	291.4	91.6	974	6	AX306529	AX306529 Sequence
5	291.4	91.6	974	6	BD131246	BD131246 Human mon
6	291	91.5	388	6	AR161375	AR161375 Sequence
7	291	91.5	388	6	AR369968	AR369968 Sequence
8	291	91.5	388	6	BD096602	BD096602 Transgeni
9	289.8	91.1	327	9	HSA388657	AJ388657 Homo sapi
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11	289.2	90.9	324	9	AF306360	AF306360 Homo sapi
12	288.2	90.6	324	9	AF146407	AF146407 Homo sapi
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14	288.2	90.6	812	9	AB064045	AB064045 Homo sapi
15	287.4	90.4	310	9	HSA408418	AJ408418 Homo sapi
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18	285.2	89.7	321	6	BD097622	BD097622 Antibody
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45	274.4	86.3	588	9	AF431052	AF431052 Homo sapi

ALIGNMENTS

RESULT 1
HSA458381
LOCUS HSA458381 318 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain variable region (IGKV gene), clone 100.
ACCESSION AJ458381
VERSION AJ458381.1 GI:20387061
KEYWORDS IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y., Valent,P., Kraft,D. and Valenta,R.

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  TITLE     Conversion of grass allergen-specific human IgE into a protective
            IgG1 antibody
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 318)
  AUTHORS   Flicker,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
            General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
            Vienna, AUSTRIA
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  Best Local Similarity   100.0%;  Pred. No. 2.4e-89;
  Matches  318;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
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Qy        301 AAGGTGGAAATCAAACGA 318
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Db        301 AAGGTGGAAATCAAACGA 318


RESULT 2
HSIGKLC5
LOCUS       HSIGKLC5                 705 bp    RNA     linear   SYN 29-MAR-2001
DEFINITION  Synthetic construct including Homo sapiens immunoglobulin kappa
            chain (clone: 5).
ACCESSION   X95747
VERSION     X95747.1  GI:1514580
KEYWORDS    constant region; immunoglobulin; kappa light chain.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Steinberger,P., Kraft,D. and Valenta,R.
  TITLE     Construction of a combinatorial IgE library from an allergic
            patient. Isolation and characterization of human IgE Fabs with
            specificity for the major timothy grass pollen allergen, Phl p 5
  JOURNAL   J. Biol. Chem. 271 (18), 10967-10972 (1996)
  MEDLINE   96210038
   PUBMED   8631916
REFERENCE   2  (bases 1 to 705)
  AUTHORS   Valenta,R.L.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &
            Experimental Pathology, General Hospital, Waehringer Guertel 18-20,
            1090 Vienna, AUSTRIA
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     misc_feature    163. .207
                     /note="FR2"
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     misc_feature    229. .324
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RESULT 3
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LOCUS       AX305000                 974 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 29 from Patent EP1158004.
ACCESSION   AX305000
VERSION     AX305000.1  GI:17644678
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Takashi,T., Katsunari,T.P. and Nobuaki,H.
  TITLE     Human monoclonal antibody against a costimulatory signal
            transduction molecule ailim and pharmaceutical use thereof
  JOURNAL   Patent: EP 1158004-A 29 28-NOV-2001;
            Japan Tobacco Inc. (JP)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match            91.6%;  Score 291.4;  DB 6;  Length 974;
  Best Local Similarity  95.0%;  Pred. No. 5.6e-81;
  Matches  301;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Qy        302 AGGTGGAAATCAAACGA 318
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Db        412 AGGTGGAAATCAAACGA 428


RESULT 4
AX306529
LOCUS       AX306529                 974 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 29 from Patent WO0187981.
ACCESSION   AX306529
VERSION     AX306529.1  GI:17645749
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tsuji,T., Tezuka,K. and Hori,N.
  TITLE     Human monoclonal antibody against a costimulatory signal
            transduction molecule ailim and pharmaceutical use thereof
  JOURNAL   Patent: WO 0187981-A 29 22-NOV-2001;
            Japan Tobacco Inc. (JP)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     5'UTR           1. .38
     CDS             39. .749
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD19048.1"
                     /db_xref="GI:17645750"
                     /db_xref="REMTREMBL:CAD19048"
                     /translation="MDMRVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTIT
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                     EDFATYYCQQANSFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN
                     FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
                     THQGLSSPVTKSFNRGEC"
     sig_peptide     39. .104
     3'UTR           750. .974
ORIGIN

  Query Match            91.6%;  Score 291.4;  DB 6;  Length 974;
  Best Local Similarity  95.0%;  Pred. No. 5.6e-81;
  Matches  301;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||

Db        112 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 171

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        172 GTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 231
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Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        232 CCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 291

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        292 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 351

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||  || || ||||| |||||||
Db        352 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTGGACGTTCGGCCAAGGGACCA 411

Qy        302 AGGTGGAAATCAAACGA 318
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Db        412 AGGTGGAAATCAAACGA 428
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RESULT 5
BD131246
LOCUS       BD131246                974 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Human monoclonal antibody against constimulation transducer
            molecule AILIM and medicinal utilization thereof.
ACCESSION   BD131246
VERSION     BD131246.1  GI:23226191
KEYWORDS    JP 2002034581-A/28.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   Tsuji,T., Tezuka,K. and Hori,N.
  TITLE     Human monoclonal antibody against constimulation transducer
            molecule AILIM and medicinal utilization thereof
  JOURNAL   Patent: JP 2002034581-A 28 05-FEB-2002;
            JAPAN TOBACCO INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002034581-A/28
            PD   05-FEB-2002
            PF   30-MAR-2001 JP 2001099508
            PI   TAKASHI TSUJI,KATSUNARI TEZUKA,NOBUAKI HORI
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61K45/
            PC   00,A61P37/08,
            PC   A61P43/00,A61P43/00,C07K16/28,C07K16/46,C07K19/00,C12N5/10, PC
              C12N15/02,
            PC
            C12P21/08,G01N33/15,G01N33/50,G01N33/53,G01N33/566,G01N33/577// PC
             (C12P21/08,C12R1:91),C12N15/00,A61K37/02,C12N5/00,C12N15/00 CC
            Human monoclonal antibody against constimulation transducer  CC
                  molecule AILIM
            CC   and medicinal utilization thereof
            FH   Key             Location/Qualifiers
            FT   5'UTR           (1). .(38)
            FT   CDS             (39). .(749)
            FT   3'UTR           (750). .(974)
            FT   sig_peptide     (39). .(104).
FEATURES              Location/Qualifiers
     source           1. .974
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             91.6%;  Score 291.4;  DB 6;  Length 974;
  Best Local Similarity   95.0%;  Pred. No. 5.6e-81;
  Matches  301;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        112 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 171

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        172 GTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 231
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Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||||||||||||||  |||||||||||||||||||||||||| ||||||||||
Db        232 CCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 291

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        292 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 351

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||  || || ||||| |||||||
Db        352 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTGGACGTTCGGCCAAGGGACCA 411

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        412 AGGTGGAAATCAAACGA 428
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RESULT 6
AR161375
LOCUS       AR161375                388 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 358 from patent US 6255458.
ACCESSION   AR161375
VERSION     AR161375.1  GI:16227235
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 388)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     High affinity human antibodies and human antibodies against digoxin
  JOURNAL   Patent: US 6255458-A 358 03-JUL-2001;
FEATURES              Location/Qualifiers
     source           1. .388
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             91.5%;  Score 291;  DB 6;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 8.4e-81;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||| ||||||||| |||||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
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Db        374 AGCTGGAGATCAAAC 388
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RESULT 7
AR369968
LOCUS       AR369968                388 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 206 from patent US 6300129.
ACCESSION   AR369968
VERSION     AR369968.1  GI:34606408
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 388)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals for producing heterologous antibodies
  JOURNAL   Patent: US 6300129-A 206 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .388
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.5%;  Score 291;  DB 6;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 8.4e-81;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388


RESULT 8
BD096602
LOCUS       BD096602                388 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Transgenic non-human animals capable of producing heterologous
            antibodies.
ACCESSION   BD096602
VERSION     BD096602.1  GI:22642190
KEYWORDS    JP 2001527386-A/129.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 388)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals capable of producing heterologous
            antibodies
  JOURNAL   Patent: JP 2001527386-A 129 25-DEC-2001;
            GENPHARM INTERNATIONAL
COMMENT     OS   Unidentified
            PN   JP 2001527386-A/129
            PD   25-DEC-2001
            PF   01-DEC-1997 JP 1998525687
            PR   02-DEC-1996 US    08/758417
            PI   NILS LONBERG,ROBERT M KAY
            PC   C12N5/00,C12N5/28,C12N5/24,C12N5/10,C07K16/00,A61K39/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Transgenic non-human animals capable of
            producing heterologous
            CC          antibodies
            FH   Key             Location/Qualifiers
            FT   source          1. .388
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .388
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             91.5%;  Score 291;  DB 6;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 8.4e-81;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388


RESULT 9
HSA388657
LOCUS       HSA388657               327 bp    mRNA    linear   PRI 22-JUL-1999
DEFINITION  Homo sapiens partial mRNA for immunoglobulin kappa chain variable
            region (IGVK gene), sample GN30.
ACCESSION   AJ388657
VERSION     AJ388657.1  GI:5578815
KEYWORDS    IgVk gene; immunoglobulin kappa chain; immunoglobulin light chain;
            variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Capello,D., Fais,F., Vivenza,D., Migliaretti,G., Chiorazzi,N.,
            Gaidano,G. and Ferrarini,M.
  TITLE     Identification of three subgroups of B-cell chronic lymphocytic
            leukemia based upon mutations of BCL-6 and IGV genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 327)
  AUTHORS   Fais,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-1999) Fais F., Clinical Immunology, Istituto
            Nazionale per la Ricerca sul Cancro, L.go R. Benzi 1, 16132, ITALY
FEATURES             Location/Qualifiers
     source          1. .327
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="B-lymphocyte"
                     /rearranged
                     /note="sample GN30"
     gene            1. .327
                     /gene="IGVK"
     CDS             <1. .>327
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                     /function="immune response"
                     /codon_start=1
                     /product="immunoglobulin kappa chain variable region"
                     /protein_id="CAB51308.1"
                     /db_xref="GI:5578816"
                     /db_xref="REMTREMBL:CAB51308"
                     /translation="DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP
                     KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPRTFGQGT
                     KVEIKRT"
ORIGIN

  Query Match             91.1%;  Score 289.8;  DB 9;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 2.1e-80;
  Matches  300;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||    || || ||||| |||||||
Db        248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCGAACGTTCGGCCAAGGGACCA 307

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        308 AGGTGGAAATCAAACGA 324


RESULT 10
AY043120
LOCUS       AY043120                322 bp    mRNA    linear   PRI 31-DEC-2001
DEFINITION  Homo sapiens MCLL047 immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AY043120
VERSION     AY043120.1  GI:18025629
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 322)
  AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
  TITLE     Ig VL gene repertoire in B cell type chronic lymphocytic leukemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 322)
  AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350
            Community Drive, Manhasset, NY 11030, USA
FEATURES             Location/Qualifiers
     source          1. .322
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /isolate="MCLL047"
                     /db_xref="taxon:9606"
                     /cell_type="B lymphocyte from patient with IgM+ chronic
                     lymphocytic leukemia (CLL)"
     CDS             <1. .>322
                     /codon_start=1
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                     /protein_id="AAK94824.1"
                     /db_xref="GI:18025630"
                     /translation="DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP
                     KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQGT
                     KVEIK"
ORIGIN

  Query Match             91.0%;  Score 289.4;  DB 9;  Length 322;
  Best Local Similarity   94.9%;  Pred. No. 2.8e-80;
  Matches  299;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||| |   || || ||||| |||||||
Db        248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTGGACGTTCGGCCAAGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
              |||||||||||||||
Db        308 AGGTGGAAATCAAAC 322


RESULT 11
AF306360
LOCUS       AF306360                324 bp    mRNA    linear   PRI 28-JUN-2001
DEFINITION  Homo sapiens clone TF2.4 immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AF306360
VERSION     AF306360.1  GI:14573216
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Pichurin,P., Guo,J., Yan,X., Rapoport,B. and McLachlan,S.M.
  TITLE     Human monoclonal autoantibodies to B-cell epitopes outside the
            thyroid peroxidase autoantibody immunodominant region
  JOURNAL   Thyroid 11 (4), 301-313 (2001)
  MEDLINE   21247463
   PUBMED   11349828
REFERENCE   2  (bases 1 to 324)
  AUTHORS   McLachlan,S.M., Rapoport,B., Pichurin,P., Guo,J. and Yan,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2000) Medicine, Cedars-Sinai Medical Center, 8700
            Beverly Blvd, B-131, Los Angeles, CA 90048, USA
FEATURES             Location/Qualifiers
     source          1. .324
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                     /db_xref="taxon:9606"
                     /clone="TF2.4"
                     /cell_type="thyroid-infiltrating lymphocytes"
     CDS             <1. .>324
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                     TPO non-immunodominant region"
                     /codon_start=1
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/product="immunoglobulin light chain variable region"
/protein_id="AAK67997.1"
/db_xref="GI:14573217"
/translation="ELVMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP
KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQGT
KVEIKR"

ORIGIN

Query Match 90.9%; Score 289.2; DB 9; Length 324;
Best Local Similarity 94.3%; Pred. No. 3.2e-80;
Matches 300; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
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Db          7 GTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 66

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
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Db         67 TGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 126

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
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Db        127 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 186

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        187 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 246

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              | |||||||||||||||||||||||||||||||||||| |  || || || || ||||||
Db        247 TTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCCTGGACGTTCGGGCAAGGGACC 306

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        307 AAGGTGGAAATCAAACGA 324
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RESULT 12
AF146407
LOCUS AF146407 324 bp mRNA linear PRI 01-FEB-2000
DEFINITION Homo sapiens antibody light chain variable region (EL-14) mRNA, partial cds.
ACCESSION AF146407
VERSION AF146407.1 GI:5081718
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS van Den Brink,E.N., Turenhout,E.A., Davies,J., Bovenschen,N., Fijnvandraat,K., Ouwehand,W.H., Peters,M. and Voorberg,J.
TITLE Human antibodies with specificity for the C2 domain of factor VIII are derived from VH1 germline genes
JOURNAL Blood 95 (2), 558-563 (2000)
MEDLINE 20094679
PUBMED 10627462
REFERENCE 2 (bases 1 to 324)
AUTHORS van den Brink,E.N. and Voorberg,J.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1999) Blood Coagulation, CLB, Sanquin Blood Supply Foundation, Plesmanlaan 125, Amsterdam 1066 CX, The Netherlands
FEATURES Location/Qualifiers
source 1. .324
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="AAD39505.1"
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/translation="DIVMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP
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ORIGIN

Query Match 90.6%; Score 288.2; DB 9; Length 324;
Best Local Similarity 94.3%; Pred. No. 6.6e-80;
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              | | | || ||||||||||||||||||||||||||||||||||||||||||||| |||
Db          7 GTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 66

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
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Db         67 TGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 126

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
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Db        127 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 186

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        187 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 246

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
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Db        247 TTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCTCACTTTCGGCGGAGGGACC 306

Qy        301 AAGGTGGAAATCAAACG 317
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Db        307 AAGGTGGAAATCAAACG 323
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RESULT 13
S59162
LOCUS S59162 433 bp mRNA linear PRI 26-JUN-2000
DEFINITION Ig V kappa =anti-single/double-stranded DNA antibody NE-13 light chain variable region [human, B-cells, mRNA Partial, 433 nt].
ACCESSION S59162
VERSION S59162.1 GI:299955
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hirabayashi,Y., Munakata,Y., Takai,O., Shibata,S., Sasaki,T. and Sano,H.
TITLE Human B-cell clones expressing lupus nephritis-associated anti-DNA idiotypes are preferentially expanded without somatic mutation
JOURNAL Scand. J. Immunol. 37 (5), 533-540 (1993)
MEDLINE 93248539
PUBMED 8387226
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 130630] from the original journal article.
This sequence comes from Fig. 6.
FEATURES Location/Qualifiers
source 1. .433
/organism="Homo sapiens"
/mol_type="mRNA"
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/cell_type="B cells"
gene 1. .>433
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CDS 1. .>433
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/note="This sequence comes from Fig. 6;
mismatches(74[Y->T],122[N->D]); conceptual translation

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                     presented here differs from translation in publication"
                     /codon_start=1
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                     /db_xref="GI:8176528"
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                     EDFATYYCQQANSFPYPFGGGTKVEIKRTVAAPSVFIFPPSD"
ORIGIN

  Query Match             90.6%;  Score 288.2;  DB 9;  Length 433;
  Best Local Similarity   94.3%;  Pred. No. 6.4e-80;
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Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db        134 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        194 CCCCTAAGCTCCTGATCTACGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
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Db        314 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTTACCCTTTCGGCGGAGGGACCA 373

Qy        302 AGGTGGAAATCAAACGA 318
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Db        374 AGGTGGAGATCAAACGA 390


RESULT 14
AB064045
LOCUS       AB064045                812 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K4.
ACCESSION   AB064045
VERSION     AB064045.1  GI:21669296
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 812)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:21669297"
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                     FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
                     THQGLSSPVTKSFNRGECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGGGSG"
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ORIGIN

  Query Match             90.6%;  Score 288.2;  DB 9;  Length 812;
  Best Local Similarity   94.3%;  Pred. No. 5.9e-80;
  Matches  299;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
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Db        314 TTGCAACTTACTATTGTCAACAGGCTAACAATTTCCCCCTCACTTTCGGCGGAGGGACCA 373

Qy        302 AGGTGGAAATCAAACGA 318
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Db        374 AGGTGGAGATCAAACGA 390


RESULT 15
HSA408418
LOCUS       HSA408418               310 bp    DNA     linear   PRI 01-AUG-2001
DEFINITION  Homo sapiens partial IGKV gene for immunoglobulin kappa chain
            variable region, clone 23.
ACCESSION   AJ408418
VERSION     AJ408418.1  GI:12655521
KEYWORDS    IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain;
            variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 310)
  AUTHORS   Harfst,E., Cooper,S., Neubauer,S., Distel,L. and Grawunder,U.
  TITLE     Normal V(D)J recombination in cells from patients with Nijmegen
            breakage syndrome
  JOURNAL   Mol. Immunol. 37 (15), 915-929 (2000)
  MEDLINE   21179652
   PUBMED   11282395
REFERENCE   2  (bases 1 to 310)
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  AUTHORS   Harfst,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2001) Harfst E., Immunologie,
            Universitaetsklinkum Ulm, Albert-Einstein-Allee 11$ D-89081 Ulm,
            GERMANY
FEATURES             Location/Qualifiers
     source          1. .310
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                     /db_xref="taxon:9606"
                     /clone="23"
                     /cell_type="B cell"
                     /tissue_type="peripheral blood lymphocytes (PBL)"
                     /rearranged
                     /note="Nijmegen breakage syndrome (NBS) patient"
     gene            1. .310
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                     /codon_start=2
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ORIGIN

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  Best Local Similarity   96.4%;  Pred. No. 1.2e-79;
  Matches  294;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db          6 AGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 65

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db         66 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 125

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        126 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 185

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        186 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 245

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
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Qy        302 AGGTG 306
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Job time : 1370.2 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 1864.96 Seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-6
Perfect score: 318
Sequence: 1 gagctcacgcagtctccatc.....ccaaggtggaaatcaaacga 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	286.6	90.1	1100	10	BF663472	BF663472 602144635
5	285	89.6	606	14	CD690290	CD690290 EST6813 h
6	283.4	89.1	558	14	CD690030	CD690030 EST6553 h
7	283.4	89.1	755	12	BG533970	BG533970 602553071
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9	282	88.7	605	14	CD688415	CD688415 EST4937 h
10	281.8	88.6	472	14	CD702614	CD702614 EST19139
11	280.2	88.1	497	14	CD696718	CD696718 EST13241
12	278.6	87.6	912	10	BF129120	BF129120 601811580
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14	275.4	86.6	561	14	CD706288	CD706288 EST22815
15	274.6	86.4	851	12	BG686018	BG686018 602638582
16	272	85.5	629	14	CD697149	CD697149 EST13672
17	271.4	85.3	421	14	CD690477	CD690477 EST7000 h
18	270.6	85.1	459	14	CD695600	CD695600 EST12123
19	268.8	84.5	903	13	BQ706785	BQ706785 AGENCOURT
20	267.2	84.0	710	14	CD695065	CD695065 EST11588
21	266.6	83.8	906	12	BG756264	BG756264 602713576
22	265.8	83.6	484	14	CD696042	CD696042 EST12565
23	265.8	83.6	486	14	CD683960	CD683960 EST480 hu
24	265.8	83.6	487	10	AW405988	AW405988 UI-HF-BL0
25	265.8	83.6	594	12	BI001311	BI001311 MR2-HN006
26	265.8	83.6	724	12	BI837410	BI837410 603086702
27	264.2	83.1	421	10	AW406227	AW406227 UI-HF-BL0
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34	262.6	82.6	677	14	CD692170	CD692170 EST8709 h
35	262.6	82.6	748	14	CB956867	CB956867 AGENCOURT
36	262.6	82.6	759	14	CB984469	CB984469 AGENCOURT
37	261	82.1	422	10	AW407904	AW407904 UI-HF-BL0
38	261	82.1	741	14	CB958688	CB958688 AGENCOURT
39	261	82.1	969	13	BU899279	BU899279 AGENCOURT
40	259.4	81.6	447	10	AW405752	AW405752 UI-HF-BL0
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43	258.4	81.3	834	12	BG679628	BG679628 602627680
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ALIGNMENTS

RESULT 1
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LOCUS BF976230 943 bp mRNA linear EST 22-JAN-2001
DEFINITION 602245105F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336225 5', mRNA sequence.
ACCESSION BF976230
VERSION BF976230.1 GI:12343445
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 943)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1208 row: j column: 02
High quality sequence stop: 721.

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FEATURES             Location/Qualifiers
     source          1. .943
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4336225"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             92.6%;  Score 294.6;  DB 10;  Length 943;
  Best Local Similarity   95.6%;  Pred. No. 2.7e-82;
  Matches  303;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db         91 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 150

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db        151 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 210

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        211 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 270

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        271 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 330

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
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Db        331 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCACACTTTTGGCCAGGGGACCA 390

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        391 AGCTGGAGATCAAACGA 407


RESULT 2
BX336281
LOCUS       BX336281                891 bp    mRNA    linear   EST 02-MAY-2003
DEFINITION  BX336281 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI026YL22 5-PRIME, mRNA sequence.
ACCESSION   BX336281
VERSION     BX336281.1  GI:30341499
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 891)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1696.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI026DF11QP1&cluster=1696.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI026DF11QP1.
FEATURES             Location/Qualifiers
     source          1. .891
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                     /db_xref="taxon:9606"
                     /clone="CS0DI026YL22"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             91.1%;  Score 289.8;  DB 13;  Length 891;
  Best Local Similarity   94.6%;  Pred. No. 8.9e-81;
  Matches  300;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db        139 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 198

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        199 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 258

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        259 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 318

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        319 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 378

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
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Db        379 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 438

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        439 AGGTGGAAATCAAACGA 455


RESULT 3
BE939490
LOCUS       BE939490                554 bp    mRNA    linear   EST 02-OCT-2000
DEFINITION  QV0-UM0093-250800-360-a09 UM0093 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE939490
VERSION     BE939490.1  GI:10467987
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 554)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
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            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV0-UM0093-250
            800-360-a09&t3=2000-08-25&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 21
            High quality sequence stop: 547.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="UM0093"
                      /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             90.6%;  Score 288.2;  DB 10;  Length 554;
  Best Local Similarity   94.3%;  Pred. No. 2.2e-80;
  Matches  299;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db         36 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 95

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db         96 GTCGGGCGAGTCAGGCTATAAGCAGCTGGTTAGCCTGGTATCAGCAGAGACCAGGGAAAG 155

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        156 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGAGGGGTCCCACCAAGGTTCA 215

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        216 GCGGCAGTGGATCTGGGACAGATTTCACCCTCACCATCAGCAGCCTGCAGCCTGAAGATT 275

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 335

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        336 AGCTGGAGATCAAACGA 352


RESULT 4
BF663472
LOCUS       BF663472               1100 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602144635F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297736 5',
            mRNA sequence.
ACCESSION   BF663472
VERSION     BF663472.1  GI:11937367
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1152  row: f  column: 09
            High quality sequence stop: 704.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4297736"
                      /tissue_type="primary B-cells from tonsils (cell line)"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_48"
                      /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             90.1%;  Score 286.6;  DB 10;  Length 1100;
  Best Local Similarity   94.0%;  Pred. No. 1.1e-79;
  Matches  298;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db         81 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 140

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db        141 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 200

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        201 CCCCTAAGCTCCTGATCTATGCTTCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 260

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        261 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 320

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||||||||||||    |||||| |||    |||||||
Db        321 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCTCACTTTCGGCGGAGGGACCA 380

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        381 AGGTGGAGATCAAACGA 397


RESULT 5
CD690290
LOCUS       CD690290               606 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST6813 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD690290
VERSION     CD690290.1  GI:32210896
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
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            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             89.6%;  Score 285;  DB 14;  Length 606;
  Best Local Similarity   93.7%;  Pred. No. 2.4e-79;
  Matches  297;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db        141 AGATGACCCAGTCTCCATCTTCTGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 200

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
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Db        201 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 260

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||||| ||||||||||
Db        261 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 320

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        321 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACTATCAGCAGCCTGCAGCCTGAAGATT 380

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||   |||||| |||   |||||||
Db        381 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCCGCCACTTTCGGCGGAGGGACCA 440

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| ||||||||
Db        441 AGGTGGAGATCAAACGA 457


RESULT 6
CD690030
LOCUS       CD690030                 558 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST6553 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD690030
VERSION     CD690030.1  GI:32210387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             89.1%;  Score 283.4;  DB 14;  Length 558;
  Best Local Similarity   93.4%;  Pred. No. 7.3e-79;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
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Db        123 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 182

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        183 GTCGGGCGAGTCAGGGTATTAGCACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 242

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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Db        243 CCCCTAAACTCCTGATCTATGCTGCATCCAATTTGCTAAGTGGGGTCCCATCAAGATTCA 302

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Db        303 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATT 362

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||     || || ||||| |||||||
Db        363 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 422

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        423 AGGTGGAAATCAAACGA 439


RESULT 7
BG533970
LOCUS       BG533970                 755 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602553071F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4663096 5',
            mRNA sequence.
ACCESSION   BG533970
VERSION     BG533970.1  GI:13525510
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1464  row: m  column: 17
            High quality sequence stop: 726.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4663096"
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                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           89.1%;  Score 283.4;  DB 12;  Length 755;
  Best Local Similarity  93.4%;  Pred. No. 8.8e-79;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Db        101 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACGGAGTCACCATCACTT 160

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||| ||||| |||||||||||||||||||||||| |||||||||
Db        161 GTCGGGCGAGTCAGGGTATCAGCAGCTGGTTAGCCTGGTATCAGCAGAAAGCAGGGAAAG 220

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        221 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 280

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        281 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 340

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||| |||||||||||  | ||||||  |||   |||||||
Db        341 TTGCAACTTACTATTGTCAACAGGGTAACAGTTTCCCTTTCACTTTCGGCGGAGGGACCA 400

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        401 AGGTGGAGATCAAACGA 417


RESULT 8
BX336280/c
LOCUS       BX336280                997 bp    mRNA    linear   EST 02-MAY-2003
DEFINITION  BX336280 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI026YL22 3-PRIME, mRNA sequence.
ACCESSION   BX336280
VERSION     BX336280.1  GI:30339485
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1696.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI026DF11NP1&cluster=1696.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI026DF11NP1.
FEATURES             Location/Qualifiers
     source          1. .997
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI026YL22"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match           89.1%;  Score 283.4;  DB 13;  Length 997;
  Best Local Similarity  92.4%;  Pred. No. 1e-78;
  Matches  293;  Conservative    4;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||:|||||||||||||||||||||||| |||||||||| ||||
Db        935 AGATGACCCAGTCTCCWTCTTCCGTGTCTGCATCTGTAGGAAACAGAGTCACCATCACTT 876

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||
Db        875 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTTTCAGCAGAAACCAGGGAAAG 816

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||: |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        815 CCCCTARGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 756

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        755 GCGGCAGTGGATCTGGGACAGATTTAAMTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 696

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||:|||:|||||||||||||||||||||||||||||||    || || ||||| |||||||
Db        695 TTGCMACTYACTATTGTCAACAGGCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 636

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        635 AGGTGGAAATCAAACGA 619


RESULT 9
CD688415
LOCUS       CD688415                605 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST4937 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD688415
VERSION     CD688415.1  GI:32207195
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
```

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ORIGIN

  Query Match             88.7%;  Score 282;  DB 14;  Length 605;
  Best Local Similarity   93.6%;  Pred. No. 2.1e-78;
  Matches  294;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          5 TCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTTGTC 64
              | || |||||||||||||| |||||||||||||| |||||||||||||||||| |||||||
Db        123 TGACCCAGTCTCCATCTTCTGTGTCTGCATCTGTTGGAGACAGAGTCACCATCACTTGTC 182

Qy         65 GGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCC 124
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        183 GGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCC 242

Qy        125 CTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCAGCG 184
              |||||||||||||||  | |||||||||||||||||||||||||| ||||||||||||||
Db        243 CTAAACTCCTGATCTCTACTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCG 302

Qy        185 GCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATTCTG 244
              |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||| ||
Db        303 GCAGTGGATCTGGGACAGATTTCACTCTCACTATCAGCAGCCTGCAGCCTGAAGATTTTG 362

Qy        245 CAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCAAGG 304
              |||||||||||||||||||| ||||||||||||||  |||||| |||    ||||||||||
Db        363 CAACTTACTATTGTCAACAGACTAACAGTTTCCCGCTCACTTTCGGCGGAGGGACCAAGG 422

Qy        305 TGGAAATCAAACGA 318
              |||| |||||||||
Db        423 TGGAGATCAAACGA 436


RESULT 10
CD702614
LOCUS       CD702614                472 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST19139 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD702614
VERSION     CD702614.1  GI:32233244
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .472
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             88.6%;  Score 281.8;  DB 14;  Length 472;
  Best Local Similarity   93.1%;  Pred. No. 2.1e-78;
  Matches  295;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||| |||||||| ||||
Db        125 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGCGTCACCATCACTT 184

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||| |||||||| |||||||||||||||||||||||||||||||||||
Db        185 GTCGGGCGAGTCAGGCTATTAGCACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 244

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||||| ||||||||||
Db        245 CCCCTAAGCTCCTGATCTATACTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 304

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        305 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 364

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||| |||||||||||||||||||||||||  |||||| |||  |||||||
Db        365 TTGCAACTTACTATGGTCAACAGGCTAACAGTTTCCCTCTCACTTTCGGCGGAGGGACCA 424

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        425 AGGTGGAGATCAAACGA 441


RESULT 11
CD696718
LOCUS       CD696718                497 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST13241 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD696718
VERSION     CD696718.1  GI:32223477
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 497)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .497
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             88.1%;  Score 280.2;  DB 14;  Length 497;
  Best Local Similarity   92.7%;  Pred. No. 7.1e-78;
  Matches  294;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||| |||||| |||||||||||||||||||| ||||
Db        120 AGATGACCCAGTCTCCATCTTCCGGGTCTGCTTCTGTAGGAGACAGAGTCACCATCACTT 179

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        180 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 239

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||  |||||| |||||||||||||||| |||||||||  ||||||||||
Db        240 CCCCTAAGCTCCTCGTCTATGCTGCATCCAGTTTGCAAGGTGGGGTCCCATCAAGGTTCA 299

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
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Db        300 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 359

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||| |||||||||||||||||||||| | |||||| |||| |||||||
Db        360 TTGCAACTTACTATGGTCAACAGGCTAACAGTTTCCCTTTCACTTTCGGCCCTGGGACCA 419

Qy        302 AGGTGGAAATCAAACGA 318
              | ||||| |||||||||
Db        420 AAGTGGATATCAAACGA 436


RESULT 12
BF129120
LOCUS       BF129120                 912 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601811580F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054530 5',
            mRNA sequence.
ACCESSION   BF129120
VERSION     BF129120.1  GI:10968160
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM894  row: p  column: 19
            High quality sequence stop: 695.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4054530"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           87.6%;  Score 278.6;  DB 10;  Length 912;
  Best Local Similarity   92.4%;  Pred. No. 3.3e-77;
  Matches  293;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||| |||||||||||||||||||| ||||
Db         72 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCCGTAGGAGACAGAGTCACCATCACTT 131

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| |||||| |||||||||||||||||||||||||||||||||||||||
Db        132 GTCGGGCGAGTCAGGATATTAGTAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 191

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||||||||||||||| |||||||||||| |||||||||||| |||||||||||
Db        192 CCCCTAAACTCCTGATCTATGCTGCATCCAGTTTACAAAGTGGGGTCCCATCAAGGTTCA 251

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db        252 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCTGAAGATT 311

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||| |||||| |||| |||||||||||| | |||||| |||| |||||||
Db        312 TTGCAACTTACCATTGTCTACAGACTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCA 371

Qy        302 AGGTGGAAATCAAACGA 318
              | ||||| ||||| |||
Db        372 AAGTGGATATCAAGCGA 388


RESULT 13
BG341803
LOCUS       BG341803                 894 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602463535F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576136 5',
            mRNA sequence.
ACCESSION   BG341803
VERSION     BG341803.1  GI:13148241
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1288  row: f  column: 09
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
     source          1. .894
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4576136"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           86.9%;  Score 276.2;  DB 12;  Length 894;
  Best Local Similarity   94.0%;  Pred. No. 1.9e-76;
  Matches  298;  Conservative    0;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         86 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 145

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||||
Db        146 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA-GGAAAG 204
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Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        205 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 264

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        265 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 324

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||| | |||||| |||| |||||||
Db        325 TTGCAACTTACTATTGTCAACAGGCTCACAGTTTCCCATTCACTTTCGGCCCTGGGACCA 384

Qy        302 AGGTGGAAATCAAACGA 318
              | ||||| |||||||||
Db        385 AAGTGGATATCAAACGA 401
```

```
RESULT 14
CD706288
LOCUS       CD706288                561 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST22815 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD706288
VERSION     CD706288.1  GI:32236918
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN
```

```
  Query Match           86.6%;  Score 275.4;  DB 14;  Length 561;
  Best Local Similarity   91.8%;  Pred. No. 2.6e-76;
  Matches  291;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        117 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 176

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||| |||||||||  |||||||||||||||| || ||||||||||||||
Db        177 GTCGGGCGAGTCAAGGTATTAGCAACTGGTTAGCCTGGTATCAACACAAACCAGGGAAAG 236

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| ||||| |||||| |||||||||||||||| ||||||||| |||||||| |
Db        237 CCCCTAAGCTCCTAATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTTA 296

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        297 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 356

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||| |||||| ||| |||||||||||||   ||| || ||||| |||||||
```

```
Db        357 TTGCAACTTACTCTTGTCAGCAGACTAACAGTTTCCCTCGCACATTCGGCCAAGGGACCA 416

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        417 AGGTGGAAATCAAACGA 433
```

```
RESULT 15
BG686018
LOCUS       BG686018                851 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602638582F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766157 5',
            mRNA sequence.
ACCESSION   BG686018
VERSION     BG686018.1  GI:13917415
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1626  row: c  column: 22
            High quality sequence stop: 851.
FEATURES             Location/Qualifiers
     source          1. .851
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4766157"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
```

```
  Query Match           86.4%;  Score 274.6;  DB 12;  Length 851;
  Best Local Similarity   93.7%;  Pred. No. 5.9e-76;
  Matches  297;  Conservative    0;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         81 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 140

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        141 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA-GGAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| || |||||||||||||||||||||||| ||||||||||
Db        200 CCCCTAAGCTCCTGATCTATGCTTCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        260 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319
```

```
Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||||||||||||||||    |||||| |||    |||||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCTCACTTTCGGCGGAGGGACCA 379

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        380 AGGTGGAGATCAAACGA 396
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Search completed: August 13, 2004, 07:13:28
Job time : 1868.96 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 207.182 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-6
Perfect score: 318
Sequence: 1 gagctcacgcagtctccatc.....ccaaggtggaaatcaaacga 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	318	100.0	318	6	ABK89642	Abk89642 DNA encod
2	291.4	91.6	974	6	AAS99473	Aas99473 Anti-huma
3	291	91.5	388	2	AAT73441	Aat73441 Human imm
4	291	91.5	388	2	AAV39239	Aav39239 Functiona
5	291	91.5	388	2	AAZ21993	Aaz21993 Partial n
6	286.4	90.1	632	7	ABZ22309	Abz22309 S. pneumo
7	285.2	89.7	321	4	AAH47735	Aah47735 Nucleotid
8	283.4	89.1	420	2	AAT73445	Aat73445 Human imm
9	283.4	89.1	420	2	AAV39293	Aav39293 Synthetic
10	283.4	89.1	420	2	AAZ22047	Aaz22047 Nucleotid
11	283.4	89.1	3819	2	AAT78825	Aat78825 Kappa lig
12	283.4	89.1	3819	2	AAV39266	Aav39266 Plasmid p
13	283.4	89.1	3819	2	AAZ22020	Aaz22020 Nucleotid
14	281.8	88.6	705	9	ADE28412	Ade28412 Human ant
15	280.8	88.3	728	7	ABT31882	Abt31882 Anti-CD40
16	280.4	88.2	321	6	ABA94337	Aba94337 MAb 63 li
17	280.2	88.1	705	9	ADE28428	Ade28428 Human ant
18	278.8	87.7	321	9	ADE28416	Ade28416 Human ant
19	277.2	87.2	321	9	ADE28432	Ade28432 Human ant
20	277	87.1	409	2	AAV39241	Aav39241 Functiona
21	277	87.1	439	2	AAT73443	Aat73443 Human imm
22	275.6	86.7	321	6	AAD46295	Aad46295 Human KDR
23	275.6	86.7	321	7	ABT23330	Abt23330 VEGF bind
24	275.6	86.7	321	9	ADD24425	Add24425 Human lig
25	275.6	86.7	321	9	ADD80802	Add80802 Human clo
26	275.4	86.6	384	2	AAT46133	Aat46133 Monoclona
27	275.4	86.6	384	2	AAT85844	Aat85844 Monoclona
28	275.4	86.6	439	2	AAZ21995	Aaz21995 Partial n
29	274	86.2	321	4	AAF75586	Aaf75586 Human ant
30	272.4	85.7	321	4	AAF75588	Aaf75588 Human ant
31	270.2	85.0	321	6	ABA94339	Aba94339 MAb 1B7 l
32	269	84.6	684	4	AAH30048	Aah30048 TRO005 ka
33	268.4	84.4	321	5	AAH68654	Aah68654 Human ant
34	268.4	84.4	321	8	ACD45318	Acd45318 Anti-Rh(D
35	267.6	84.2	321	5	AAH26789	Aah26789 Anti-huma
36	267	84.0	322	4	AAF55238	Aaf55238 DNA seque
37	267	84.0	322	4	AAF55231	Aaf55231 Nucleotid
38	266.8	83.9	321	5	AAH68701	Aah68701 Human ant
39	266.8	83.9	321	8	ACD45365	Acd45365 Anti-Rh(D
40	265.4	83.5	321	6	AAD46301	Aad46301 Human KDR
41	265.4	83.5	321	7	ABT23336	Abt23336 VEGF bind
42	265.4	83.5	321	9	ADD24437	Add24437 Human lig
43	265.4	83.5	321	9	ADD80814	Add80814 Human KDR
44	264.8	83.3	333	5	AAH74664	Aah74664 Nucleotid
45	264.8	83.3	426	7	ADA43064	Ada43064 Human ant

ALIGNMENTS

RESULT 1
ABK89642
ID ABK89642 standard; DNA; 318 BP.
XX
AC ABK89642;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 100 light chain.
XX
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .318
FT /*tag= a
FT /product= "Fab clone 100 heavy chain"
FT /transl_except= (pos:193. .195, aa:Tyr)
FT misc_feature 7. .63
FT /*tag= b
FT /note= "FR1 region"
FT misc_feature 64. .96
FT /*tag= c
FT /note= "CDR1 region"
FT misc_feature 97. .141
FT /*tag= d
FT /note= "FR2 region"
FT misc_feature 142. .162
FT /*tag= e
FT /note= "CDR2 region"
FT misc_feature 163. .258
FT /*tag= f
FT /note= "FR3 region"
FT misc_feature 259. .285
FT /*tag= g
FT /note= "CDR3 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.

XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR P-PSDB; ABG30450.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 35-36; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 100 light chain protein of the
CC invention
XX
SQ Sequence 318 BP; 80 A; 81 C; 81 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 318; DB 6; Length 318;
Best Local Similarity 100.0%; Pred. No. 6.9e-93;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        301 AAGGTGGAAATCAAACGA 318
```

RESULT 2
AAS99473
ID AAS99473 standard; cDNA; 974 BP.
XX
AC AAS99473;
XX
DT 12-MAR-2002 (first entry)
XX
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.
XX
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation; ss;
KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX
OS Homo sapiens.
XX
PN WO200187981-A2.
XX
PD 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-JP004035.
XX
PR 18-MAY-2000; 2000JP-00147116.
PR 30-MAR-2001; 2001JP-00099508.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Tsuji T, Tezuka K, Hori N;
XX
DR WPI; 2002-075313/10.
DR P-PSDB; AAU74297.
XX
PT New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
PS Claim 45; Page 267-270; 300pp; English.
XX
CC The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AILIM, for modulating proliferation
CC of AILIM-expressing cells, for modulating production of a cytokine from
CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AILIM-expressing cells and/or immune cytolysis or apoptosis of
CC AILIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AILIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAS99444-AAS99477 represent anti-human
CC AILIM monoclonal antibody coding sequences and PCR primers of the
CC invention
XX
SQ Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 U; 0 Other;

Query Match 91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity 95.0%; Pred. No. 4.6e-84;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        112 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 171

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        172 GTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 231
```

```
Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||||||||||||||||  ||||||||||||||||||||||||||| ||||||||||
Db        232 CCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 291

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        292 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 351

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||||||||||||||  || || ||||| |||||||
Db        352 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTGGACGTTCGGCCAAGGGACCA 411

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||||||||||||
Db        412 AGGTGGAAATCAAACGA 428
```

RESULT 3
AAT73441
ID AAT73441 standard; DNA; 388 BP.
XX
AC AAT73441;
XX
DT 03-DEC-1997 (first entry)
XX
DE Human immunoglobulin light chain variable region partial transcript.
XX
KW Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US016433.
XX
PR 10-OCT-1995; 95US-00544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Claim 44; Page 255; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M
CC -1 for binding to a predetermined human antigen. The present sequence
CC represents a human light chain variable region partial nucleotide
CC sequence, 10C5 kappa, which encodes an amino acid sequence from a claimed
CC immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies
CC may be used in therapeutic and diagnostic applications, especially for
CC the treatment of human diseases. These antibodies reduce activity of CD4
CC cells and reduce undesirable autoimmune reactions, inflammatory response
CC and transplant rejection. Transgenic animals are capable of producing
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. These animals produce a first Ig type that is necessary for
CC antigen-stimulated B-cell maturation and can switch to encode and produce
CC one or more subsequent heterologous isotypes
XX
SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

```
  Query Match             91.5%;  Score 291;  DB 2;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 4.3e-84;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;
```

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| |||||||| |||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388
```

RESULT 4
AAV39239
ID AAV39239 standard; DNA; 388 BP.
XX
AC AAV39239;
XX
DT 18-DEC-1998 (first entry)
XX
DE Functional Kappa transcript isolated from transgenic cell line 10C5.
XX
KW Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021803.
XX
PR 02-DEC-1996; 96US-00758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to prevent
PT efflux of neutrophils from vasculature, and treat reperfusion injury.
XX
PS Example 41; Page 304; 452pp; English.
XX
CC AAV39232-41 represent functional transcripts of a human IgGKappa anti-CD4
CC antibody. The sequences are isolated from 5 different transgenic mouse
CC hybridoma cell lines. The specification describes transgenic non-human
CC animals, especially a mouse, which are capable of producing a human
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a

```
CC   heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC   recombination. The transgenes include a heavy chain transgene comprising
CC   at least one V, D and J gene segment, and one constant region gene
CC   segment. The immunoglobulin (Ig) light chain transgene comprises at least
CC   one V and J gene segment and one constant region gene segment. The gene
CC   segments are heterologous to the transgenic animal. The antibody can be
CC   used to prevent efflux of neutrophils from vasculature. It can also be
CC   used to treat reperfusion injury. CD4 binding antibodies are used to
CC   reduce undesirable autoimmune reactions, inflammatory responses and
CC   rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC   tissue damage and prolong survival in animal models of acute adult
CC   respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC   anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC   septic shock, allergic reactions (e.g. asthma) and cystic fibrosis
XX
SQ   Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

  Query Match             91.5%;  Score 291;  DB 2;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 4.3e-84;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388


RESULT 5
AAZ21993
ID   AAZ21993 standard; DNA; 388 BP.
XX
AC   AAZ21993;
XX
DT   24-NOV-1999  (first entry)
XX
DE   Partial nucleotide sequence for a functional transcript 10C5-kappa.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   transgenic mouse; human heavy chain transgene; digoxin; PCR primer;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005535.
XX
PR   13-MAR-1998;   98US-00042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Fishwild DM,  Ball WJ;
XX
DR   WPI; 1999-551219/46.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies.
XX
PS   Example 41; Page 305; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable amount
CC   of an immunoglobulin that specifically binds digoxin or Shinga-like
CC   toxin. B cells from transgenic animals can be used to generate hybridomas
CC   expressing monoclonal high affinity human sequence antibodies. Antibodies
CC   produced from the transgenic animals of the invention can be used to
CC   treat human diseases, e.g. autoimmune diseases, cancer, infectious
CC   disease, transplant rejection, blood disorders such as coagulation
CC   disorders and other diseases. The present sequence represents a partial
CC   nucleotide sequence for a functional transcript used in the course of the
CC   invention
XX
SQ   Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

  Query Match             91.5%;  Score 291;  DB 2;  Length 388;
  Best Local Similarity   95.2%;  Pred. No. 4.3e-84;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388


RESULT 6
ABZ22309
ID   ABZ22309 standard; DNA; 632 BP.
XX
AC   ABZ22309;
XX
DT   20-MAR-2003  (first entry)
XX
DE   S. pneumoniae PPS-3 antibody 3H1 light chain DNA sequence SEQ ID NO:4.
XX
KW   Antipneumococcal; antibody; monoclonal antibody; infection; PPS-3;
KW   Streptococcus pneumoniae; capsular polysaccharide; gene; ds.
XX
OS   Streptococcus pneumoniae.
OS   Synthetic.
```

XX
PN WO200292017-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-US018363.
XX
PR 16-MAY-2001; 2001US-0291492P.
XX
PA (PIRO/) PIROFSKY L.
PA (ZHON/) ZHONG Z.
PA (CHAN/) CHANG Q.
XX
PI Pirofsky L, Zhong Z, Chang Q;
XX
DR WPI; 2003-120598/11.
XX
PT New antibody or its antigen-binding fragment that specifically binds the
PT capsular polysaccharide of Streptococcus pneumoniae serotype 3, useful
PT for treating, inhibiting or preventing S. pneumoniae infections.
XX
PS Claim 13; Fig 6B; 56pp; English.
XX
CC The present invention describes an antibody or its antigen-binding
CC fragment (I) that specifically binds the capsular polysaccharide of
CC Streptococcus pneumoniae serotype 3 (S. pneumoniae PPS-3), comprising a
CC heavy and/or light chain amino acid sequence. (I) has antibacterial
CC activity and can be used in vaccines. The anti-S. pneumoniae PPS-3
CC antibody or its antigen-binding fragment is useful for treating,
CC inhibiting or preventing S. pneumoniae infections or conditions or
CC disorders caused by the infection. Methods from the present invention can
CC be used for preventing or reducing the severity of conditions or
CC disorders caused by S. pneumoniae serotype 3 infection, or for increasing
CC the resistance of a subject to infection by S. pneumoniae serotype 3. The
CC present sequence represents a S. pneumoniae PPS-3 antibody light chain
CC DNA sequence from the present invention
XX
SQ Sequence 632 BP; 165 A; 175 C; 159 G; 133 T; 0 U; 0 Other;

Query Match 90.1%; Score 286.4; DB 7; Length 632;
Best Local Similarity 94.9%; Pred. No. 1.6e-82;
Matches 296; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          7 ACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTTGTCGG 66
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         12 ACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG 71

Qy         67 GCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCT 126
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db         72 GCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCT 131

Qy        127 AAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCAGCGGC 186
              || |||||||||||  ||||||| |||||||||||||||||| ||||||||||||||||
Db        132 AAGCTCCTGATCTATGTTGCATCCCGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGC 191

Qy        187 AGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATTCTGCA 246
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||
Db        192 AGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA 251

Qy        247 ACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCAAGGTG 306
              |||||||||||||||||||||||||||||||    || || ||||| ||||||||||||
Db        252 ACTTACTATTGTCAACAGGCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCAAGGTG 311

Qy        307 GAAATCAAACGA 318
              ||||||||||||
Db        312 GAAATCAAACGA 323
```

RESULT 7
AAH47735
ID AAH47735 standard; DNA; 321 BP.
XX
AC AAH47735;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of seq Id No. 78.
XX
KW Gene library; immunoglobulin; antibody library; human; ds.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-JP001298.
XX
PR 22-FEB-2000; 2000JP-00050543.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
DR WPI; 2001-565420/63.
DR P-PSDB; AAG65571.
XX
PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
PS Examples; p 151; 181pp; Japanese.
XX
CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
SQ Sequence 321 BP; 80 A; 85 C; 80 G; 76 T; 0 U; 0 Other;

Query Match 89.7%; Score 285.2; DB 4; Length 321;
Best Local Similarity 94.3%; Pred. No. 3.1e-82;
Matches 296; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||| ||||||   ||||||  |||  |||||||
Db        248 TTGCAACTTACTATTGTCAACAGGCTAACAATTTCCCCCTCACTTTCGGCGGAGGGACCA 307

Qy        302 AGGTGGAAATCAAA 315
              ||||||| ||||||
Db        308 AGGTGGAGATCAAA 321
```

RESULT 8
AAT73445

ID AAT73445 standard; DNA; 420 BP.
XX
AC AAT73445;
XX
DT 03-DEC-1997 (first entry)
XX
DE Human immunoglobulin light chain variable region partial transcript.
XX
KW Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US016433.
XX
PR 10-OCT-1995; 95US-00544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Claim 45; Page 272-273; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M
CC -1 for binding to a predetermined human antigen. The present sequence
CC represents a human light chain variable region partial nucleotide
CC sequence, LC6G5, which encodes an amino acid sequence from a claimed
CC immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies
CC may be used in therapeutic and diagnostic applications, especially for
CC the treatment of human diseases. These antibodies reduce activity of CD4
CC cells and reduce undesirable autoimmune reactions, inflammatory response
CC and transplant rejection. Transgenic animals are capable of producing
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. These animals produce a first Ig type that is necessary for
CC antigen-stimulated B-cell maturation and can switch to encode and produce
CC one or more subsequent heterologous isotypes
XX
SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;

Query Match 89.1%; Score 283.4; DB 2; Length 420;
Best Local Similarity 93.4%; Pred. No. 1.3e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         80 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 139

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| ||||||||| |||||||||||||||||||| |||||||| ||||
Db        140 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db        200 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        260 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 379
```

```
Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        380 AGCTGGAGATCAAACGA 396
```

RESULT 9
AAV39293
ID AAV39293 standard; DNA; 420 BP.
XX
AC AAV39293;
XX
DT 18-DEC-1998 (first entry)
XX
DE Synthetic kappa light chain sequence LC6G5.
XX
KW Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021803.
XX
PR 02-DEC-1996; 96US-00758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to prevent
PT efflux of neutrophils from vasculature, and treat reperfusion injury.
XX
PS Example 42; Page 324-325; 452pp; English.
XX
CC The present sequence represents a synthetic kappa light sequence (created
CC using oligonucleotides AAV39267-78). This synthetic sequence differs from
CC natural sequences in that strings of repeated oligonucleotides are
CC interrupted (to facilitate oligonucleotide synthesis and PCR
CC amplification), optimal translation initiation sites are incorporated and
CC HindII sites were engineered upstream of the translation initiation
CC sites. The sequence is used to make plasmid pHC6G5, which is used in the
CC construction of minigenes for expression of IgGkappa anti-CD4 antibodies,
CC in the transgenic mouse of the invention. The specification describes
CC transgenic non-human animals, especially a mouse, which are capable of
CC producing a human heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. The transgenic animals have human heavy and
CC light chain transgenes. The transgenes are capable of functionally
CC rearranging a heterologous diversity (D) gene in a variable-diversity-
CC junction (V-D-J) recombination. The transgenes include a heavy chain
CC transgene comprising at least one V, D and J gene segment, and one
CC constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions,
CC inflammatory responses and rejection of transplanted organs. The anti-IL-
CC 8 antibodies can reduce tissue damage and prolong survival in animal
CC models of acute adult respiratory distress syndrome (ARDS) and acid
CC induced lung injury. The anti-IL-8 antibodies can also be used for the
CC treatment of vasculitis, septic shock, allergic reactions (e.g. asthma)
CC and cystic fibrosis

```
XX
SQ   Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;

  Query Match             89.1%;  Score 283.4;  DB 2;  Length 420;
  Best Local Similarity   93.4%;  Pred. No. 1.3e-81;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         80 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 139

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| |||||||| ||||
Db        140 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db        200 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        260 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 379

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        380 AGCTGGAGATCAAACGA 396


RESULT 10
AAZ22047
ID   AAZ22047 standard; DNA; 420 BP.
XX
AC   AAZ22047;
XX
DT   24-NOV-1999  (first entry)
XX
DE   Nucleotide sequence of LC6G5.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   transgenic mouse; human heavy chain transgene; digoxin;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Synthetic.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005535.
XX
PR   13-MAR-1998;   98US-00042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Fishwild DM,  Ball WJ;
XX
DR   WPI; 1999-551219/46.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies.
XX
PS   Example 42; Page 325-326; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable amount
CC   of an immunoglobulin that specifically binds digoxin or Shinga-like
CC   toxin. B cells from transgenic animals can be used to generate hybridomas
CC   expressing monoclonal high affinity human sequence antibodies. Antibodies
CC   produced from the transgenic animals of the invention can be used to
CC   treat human diseases, e.g. autoimmune diseases, cancer, infectious
CC   disease, transplant rejection, blood disorders such as coagulation
CC   disorders and other diseases. The present sequence is used in the course
CC   of the invention
XX
SQ   Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;

  Query Match             89.1%;  Score 283.4;  DB 2;  Length 420;
  Best Local Similarity   93.4%;  Pred. No. 1.3e-81;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         80 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 139

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| |||||||| ||||
Db        140 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db        200 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        260 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 379

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        380 AGCTGGAGATCAAACGA 396


RESULT 11
AAT78825
ID   AAT78825 standard; DNA; 3819 BP.
XX
AC   AAT78825;
XX
DT   23-JAN-1998  (first entry)
XX
DE   Kappa light chain plasmid pLC6G5.
XX
KW   Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW   transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW   transplant rejection; immunoglobulin; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9713852-A1.
XX
PD   17-APR-1997.
XX
PF   10-OCT-1996;   96WO-US016433.
XX
PR   10-OCT-1995;   95US-00544404.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Kay RM;
XX
DR   WPI; 1997-235888/21.
XX
```

PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Example 42; Page 266-268; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M
CC -1 for binding to a predetermined human antigen. The present sequence
CC represents the kappa light chain plasmid pLC6G5 which includes the kappa
CC constant region and polyadenylation site. Anti- CD4 antibodies may be
CC used in therapeutic and diagnostic applications, especially for the
CC treatment of human diseases. These antibodies reduce activity of CD4
CC cells and reduce undesirable autoimmune reactions, inflammatory response
CC and transplant rejection. Transgenic animals are capable of producing
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. These animals produce a first Ig type that is necessary for
CC antigen-stimulated B-cell maturation and can switch to encode and produce
CC one or more subsequent heterologous isotypes
XX
SQ Sequence 3819 BP; 947 A; 1015 C; 912 G; 945 T; 0 U; 0 Other;

Query Match 89.1%; Score 283.4; DB 2; Length 3819;
Best Local Similarity 93.4%; Pred. No. 3.1e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2513 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 2572

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| |||||||| |||||||||||||||||| |||||||| ||||
Db       2573 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 2632

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||| ||||| ||||||||||
Db       2633 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 2692

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       2693 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 2752

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||
Db       2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 2812

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db       2813 AGCTGGAGATCAAACGA 2829
```

RESULT 12
AAV39266
ID AAV39266 standard; DNA; 3819 BP.
XX
AC AAV39266;
XX
DT 18-DEC-1998 (first entry)
XX
DE Plasmid pLC6G5 nucleotide sequence.
XX
KW Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021803.
XX
PR 02-DEC-1996; 96US-00758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to prevent
PT efflux of neutrophils from vasculature, and treat reperfusion injury.
XX
PS Example 42; Page 317-319; 452pp; English.
XX
CC The present sequence represents a plasmid, pLC6G5, which contains a
CC synthetic kappa light chain sequence (created using oligonucleotide
CC AAV39244-65). This synthetic sequence differs from natural sequences in
CC that strings of repeated oligonucleotides are interrupted (to facilitate
CC oligonucleotide synthesis and PCR amplification), optimal translation
CC initiation sites are incorporated and HindII sites were engineered
CC upstream of the translation initiation sites. The plasmid is used in the
CC construction of minigenes for expression of IgGkappa anti-CD4 antibodies,
CC in the transgenic mouse of the invention. The specification describes
CC transgenic non-human animals, especially a mouse, which are capable of
CC producing a human heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. The transgenic animals have human heavy and
CC light chain transgenes. The transgenes are capable of functionally
CC rearranging a heterologous diversity (D) gene in a variable-diversity-
CC junction (V-D-J) recombination. The transgenes include a heavy chain
CC transgene comprising at least one V, D and J gene segment, and one
CC constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions,
CC inflammatory responses and rejection of transplanted organs. The anti-IL-
CC 8 antibodies can reduce tissue damage and prolong survival in animal
CC models of acute adult respiratory distress syndrome (ARDS) and acid
CC induced lung injury. The anti-IL-8 antibodies can also be used for the
CC treatment of vasculitis, septic shock, allergic reactions (e.g. asthma)
CC and cystic fibrosis
XX
SQ Sequence 3819 BP; 947 A; 1015 C; 912 G; 945 T; 0 U; 0 Other;

Query Match 89.1%; Score 283.4; DB 2; Length 3819;
Best Local Similarity 93.4%; Pred. No. 3.1e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2513 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 2572

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| |||||||| |||||||||||||||||| |||||||| ||||
Db       2573 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 2632

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||| ||||| ||||||||||
Db       2633 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 2692

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       2693 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 2752

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||
Db       2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 2812

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
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Db       2813 AGCTGGAGATCAAACGA 2829


RESULT 13
AAZ22020
ID   AAZ22020 standard; DNA; 3819 BP.
XX
AC   AAZ22020;
XX
DT   24-NOV-1999  (first entry)
XX
DE   Nucleotide sequence of plasmid pLC6G5.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   transgenic mouse; human heavy chain transgene; digoxin;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Synthetic.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005535.
XX
PR   13-MAR-1998;   98US-00042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Fishwild DM,  Ball WJ;
XX
DR   WPI; 1999-551219/46.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies.
XX
PS   Example 42; Page 318-320; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable amount
CC   of an immunoglobulin that specifically binds digoxin or Shinga-like
CC   toxin. B cells from transgenic animals can be used to generate hybridomas
CC   expressing monoclonal high affinity human sequence antibodies. Antibodies
CC   produced from the transgenic animals of the invention can be used to
CC   treat human diseases, e.g. autoimmune diseases, cancer, infectious
CC   disease, transplant rejection, blood disorders such as coagulation
CC   disorders and other diseases. The present sequence is used in the course
CC   of the invention
XX
SQ   Sequence 3819 BP; 947 A; 1015 C; 912 G; 945 T; 0 U; 0 Other;

  Query Match            89.1%;  Score 283.4;  DB 2;  Length 3819;
  Best Local Similarity   93.4%;  Pred. No. 3.1e-81;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2513 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 2572

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||| |||||||| |||||||||||||||||||| |||||||| ||||
Db       2573 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 2632

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db       2633 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 2692

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       2693 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 2752

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||
Db       2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 2812

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db       2813 AGCTGGAGATCAAACGA 2829


RESULT 14
ADE28412
ID   ADE28412 standard; cDNA; 705 BP.
XX
AC   ADE28412;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human anti-CD40 antibody 10-8-3 variable region light chain cDNA.
XX
KW   anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW   immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW   bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW   human; variable region light chain; ss; gene; 10-8-3.
XX
OS   Homo sapiens.
XX
PN   WO2003040170-A2.
XX
PD   15-MAY-2003.
XX
PF   08-NOV-2002; 2002WO-US036107.
XX
PR   09-NOV-2001; 2001US-0348980P.
XX
PA   (PFIZ ) PFIZER PROD INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Bedian V,  Gladue RP,  Corvalan J,  Jia X,  Feng X;
XX
DR   WPI; 2003-441521/41.
DR   P-PSDB; ADE28413.
XX
PT   New chimeric or human monoclonal antibody or its antigen-binding portion
PT   that specifically binds to and activates human CD40, useful for enhancing
PT   an immune response in a human, or treating cancer, HIV, neutropenia or
PT   viral infections.
XX
PS   Claim 24; SEQ ID NO 19; 177pp; English.
XX
CC   The invention relates to a novel chimeric or human monoclonal antibody or
CC   its antigen-binding portion that specifically binds to and activates
CC   human CD40. The anti-CD40 antibody of the invention demonstrates
CC   cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC   activities and may be useful for treating a hyperproliferative disorder
CC   such as cancer, viral and bacterial infection or genetic, primary or
CC   combined immunodeficiency conditions including neutropenia or HIV
CC   infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC   in a biological sample in vitro or in vivo, as well as during gene
CC   therapy procedures. The current sequence is that of the human anti-CD40
CC   antibody variable region light chain cDNA of the invention.
XX
SQ   Sequence 705 BP; 172 A; 201 C; 179 G; 153 T; 0 U; 0 Other;

  Query Match            88.6%;  Score 281.8;  DB 9;  Length 705;
  Best Local Similarity   93.1%;  Pred. No. 5.3e-81;
  Matches  295;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
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Db         68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 127

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||  |||||||| ||||||||||||||||||||||||||||||||||||
Db        128 GTCGGGCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||||||||||| |||||||| ||| |||||||||||||||||| ||||||||||
Db        188 CCCCTAAACTCCTGATTTATTCTGCCTCCGGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        248 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 307

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||| || |||||||||| |||||| |||   |||||||
Db        308 TTGCAACTTACTATTGTCAACAGACTGACAGTTTCCCGCTCACTTTCGGCGGCGGGACCA 367

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        368 AGGTGGAGATCAAACGA 384
```

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RESULT 15
ABT31882
ID   ABT31882 standard; DNA; 728 BP.
XX
AC   ABT31882;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Anti-CD40 monoclonal antibody related DNA SEQ ID No 65.
XX
KW   Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
KW   human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
KW   dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
KW   immunoactivator; anti-tumour agent; immunosuppressant; allergy;
KW   autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
KW   ds.
XX
OS   Unidentified.
XX
PN   WO200288186-A1.
XX
PD   07-NOV-2002.
XX
PF   26-APR-2002; 2002WO-JP004292.
XX
PR   27-APR-2001; 2001WO-US013672.
PR   11-MAY-2001; 2001JP-00142482.
PR   05-OCT-2001; 2001JP-00310535.
PR   26-OCT-2001; 2001US-00040244.
XX
PA   (KIRI ) KIRIN BEER KK.
XX
PI   Mikayama T,  Yoshida H,  Force WR,  Chen X,  Takahashi N;
XX
DR   WPI; 2003-120463/11.
DR   P-PSDB; ABJ36940.
XX
PT   Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
PT   or functional fragment, is useful in the treatment of e.g. autoimmune
PT   diseases or cancer.
XX
PS   Claim 16; Page 59-60; 94pp; Japanese.
XX
CC   The invention relates to an antibody to human CD40, or its functional
CC   fragment, has at least one of the following properties: acting on
CC   dendritic cells to produce IL-12 in the presence of LPS
CC   (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
CC   cells to activate maturity of the dendritic cells with high G28-5
CC   antibody; and activating CD95 expression with high G28-5 antibody against
CC   B cell line. Such antibodies or functional fragments can be used as
CC   immunoactivators, anti-tumour agents, immunosuppressants, and as remedies
CC   for autoimmune diseases, allergy or coagulation factor VIII inhibitors
CC   syndrome. This polynucleotide sequence represents a coding DNA sequence
CC   relating to the anti-CD40 monoclonal antibody of the invention
XX
SQ   Sequence 728 BP; 183 A; 201 C; 195 G; 149 T; 0 U; 0 Other;

  Query Match             88.3%;  Score 280.8;  DB 7;  Length 728;
  Best Local Similarity   93.0%;  Pred. No. 1.1e-80;
  Matches  294;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||| |||||||||||||||||||||||| ||||
Db        132 AGATGACCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGAGTCACCATCACTT 191

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        192 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 251

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||| |||||||||||||||||||||| ||||||||||
Db        252 CCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 311

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Db        312 GCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 371

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||    || || ||||| |||||||
Db        372 TTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTCGGCCAAGGGACCA 431

Qy        302 AGGTGGAAATCAAACG 317
              ||||||| ||||||||
Db        432 AGGTGGAGATCAAACG 447
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Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	318	100.0	318	15	US-10-027-725A-6	Sequence 6, Appli
2	291.4	91.6	974	9	US-09-859-053-29	Sequence 29, Appl
3	286.2	90.0	322	16	US-10-309-762-224	Sequence 224, App
4	281.8	88.6	705	13	US-10-292-088-23	Sequence 23, Appl
5	280.8	88.3	728	9	US-09-844-684-15	Sequence 15, Appl
6	280.8	88.3	728	15	US-10-040-244-15	Sequence 15, Appl
7	280.8	88.3	728	17	US-10-693-629-65	Sequence 65, Appl
8	280.4	88.2	321	15	US-10-324-493-21	Sequence 21, Appl
9	280.2	88.1	705	13	US-10-292-088-47	Sequence 47, Appl
10	279.8	88.0	322	12	US-10-269-711-28	Sequence 28, Appl
11	279.8	88.0	322	15	US-10-041-860-85	Sequence 85, Appl
12	279.8	88.0	322	17	US-10-665-383-63	Sequence 63, Appl
13	278.8	87.7	321	13	US-10-292-088-19	Sequence 19, Appl
14	278.2	87.5	322	12	US-10-269-711-16	Sequence 16, Appl
15	277.6	87.3	716	9	US-09-844-684-13	Sequence 13, Appl
16	277.6	87.3	716	15	US-10-040-244-13	Sequence 13, Appl
17	277.2	87.2	321	13	US-10-292-088-43	Sequence 43, Appl
18	276.6	87.0	322	12	US-10-269-711-24	Sequence 24, Appl
19	275.6	86.7	321	15	US-10-091-300-32	Sequence 32, Appl
20	275	86.5	322	12	US-10-269-711-8	Sequence 8, Appli
21	275	86.5	322	16	US-10-309-762-213	Sequence 213, App
22	275	86.5	322	16	US-10-309-762-215	Sequence 215, App
23	275	86.5	322	16	US-10-309-762-228	Sequence 228, App
24	275	86.5	322	16	US-10-309-762-238	Sequence 238, App
25	272.2	85.6	381	16	US-10-309-762-111	Sequence 111, App
26	271.8	85.5	322	12	US-10-269-711-12	Sequence 12, Appl
27	271.8	85.5	322	12	US-10-269-711-36	Sequence 36, Appl
28	270.2	85.0	321	15	US-10-324-493-25	Sequence 25, Appl
29	270.2	85.0	322	12	US-10-269-711-32	Sequence 32, Appl
30	270.2	85.0	322	12	US-10-269-711-44	Sequence 44, Appl
31	268.4	84.4	321	10	US-09-848-798-109	Sequence 109, App
32	267.6	84.2	321	13	US-10-221-529-3	Sequence 3, Appli
33	267	84.0	322	13	US-09-948-939-12	Sequence 12, Appl
34	266.8	83.9	321	10	US-09-848-798-199	Sequence 199, App
35	265.4	83.5	321	15	US-10-091-300-44	Sequence 44, Appl
36	264.8	83.3	333	15	US-10-203-754A-23	Sequence 23, Appl
37	264.8	83.3	426	17	US-10-469-304-22	Sequence 22, Appl
38	264.8	83.3	900	15	US-10-203-754A-27	Sequence 27, Appl
39	264.8	83.3	900	15	US-10-203-754A-37	Sequence 37, Appl
40	264.4	83.1	321	10	US-09-851-614-1	Sequence 1, Appli
41	264.4	83.1	321	15	US-10-035-637-1	Sequence 1, Appli
42	264.2	83.1	384	16	US-10-389-221-10	Sequence 10, Appl
43	263.6	82.9	321	10	US-09-848-798-98	Sequence 98, Appl
44	263.6	82.9	321	10	US-09-848-798-102	Sequence 102, App
45	263.6	82.9	321	10	US-09-848-798-218	Sequence 218, App

ALIGNMENTS

RESULT 1
US-10-027-725A-6
; Sequence 6, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-6

Query Match 100.0%; Score 318; DB 15; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.9e-96;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
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Db        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        301 AAGGTGGAAATCAAACGA 318
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RESULT 2
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match 91.6%; Score 291.4; DB 9; Length 974;
Best Local Similarity 95.0%; Pred. No. 4.6e-87;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        112 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 171

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        172 GTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 231

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||||||||||||||  |||||||||||||||||||||||||| ||||||||||
Db        232 CCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 291

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        292 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 351

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||  || || ||||| |||||||
Db        352 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTGGACGTTCGGCCAAGGGACCA 411

Qy        302 AGGTGGAAATCAAACGA 318
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Db        412 AGGTGGAAATCAAACGA 428
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RESULT 3
US-10-309-762-224
; Sequence 224, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-224

Query Match 90.0%; Score 286.2; DB 16; Length 322;
Best Local Similarity 94.3%; Pred. No. 1.8e-85;
Matches 297; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||| |||||||||||| |||||||||||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTCTCACTTTCGGCCCTGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
              ||||| |||||||
Db        308 AAGTGGATATCAAAC 322
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RESULT 4
US-10-292-088-23
; Sequence 23, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147

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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 705
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-292-088-23

  Query Match             88.6%;  Score 281.8;  DB 13;  Length 705;
  Best Local Similarity   93.1%;  Pred. No. 6.8e-84;
  Matches  295;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 127

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||  ||||||||| |||||||||||||||||||||||||||||||||||
Db        128 GTCGGGCGAGTCAGCCTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||||||||||| |||||||| ||| ||||||||||||||||||| ||||||||||
Db        188 CCCCTAAACTCCTGATTTATTCTGCCTCCGGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        248 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 307

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||| || ||||||||||   |||||| |||    |||||||
Db        308 TTGCAACTTACTATTGTCAACAGACTGACAGTTTCCCGCTCACTTTCGGCGGCGGGACCA 367

Qy        302 AGGTGGAAATCAAACGA 318
              ||||||| |||||||||
Db        368 AGGTGGAGATCAAACGA 384


RESULT 5
US-09-844-684-15
; Sequence 15, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
;  APPLICANT: GEMINI SCIENCE, INC.
;  APPLICANT:  LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
;  TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
;  FILE REFERENCE: 21286/0276339
;  CURRENT APPLICATION NUMBER: US/09/844,684
;  CURRENT FILING DATE:  2001-04-27
;  PRIOR APPLICATION NUMBER: US 60/200,601
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-844-684-15

  Query Match             88.3%;  Score 280.8;  DB 9;  Length 728;
  Best Local Similarity   93.0%;  Pred. No. 1.5e-83;
  Matches  294;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db        132 AGATGACCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGAGTCACCATCACTT 191

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        192 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 251

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||| |||||||||||||||||||| ||||||||||
Db        252 CCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 311

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Db        312 GCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 371

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||     || || ||||| |||||||
Db        372 TTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTCGGCCAAGGGACCA 431

Qy        302 AGGTGGAAATCAAACG 317
              ||||||| ||||||||
Db        432 AGGTGGAGATCAAACG 447


RESULT 6
US-10-040-244-15
; Sequence 15, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
;  APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;  APPLICANT:  FORCE, WALKER F.
;  APPLICANT:  TAKAHASHI, NOBUAKI
;  APPLICANT:  MIKAYAMA, TOSHIFUMI
;  TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBO
;  FILE REFERENCE: 021286/0272501
;  CURRENT APPLICATION NUMBER: US/10/040,244
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: 60/200,601
;  PRIOR FILING DATE: 2000-4-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13672
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: 09/844,684
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 15
;   LENGTH: 728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-040-244-15

  Query Match             88.3%;  Score 280.8;  DB 15;  Length 728;
  Best Local Similarity   93.0%;  Pred. No. 1.5e-83;
  Matches  294;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db        132 AGATGACCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGAGTCACCATCACTT 191

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        192 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 251

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||| |||||||||||||||||||| ||||||||||
Db        252 CCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 311

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Db        312 GCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 371

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||     || || ||||| |||||||
Db        372 TTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTCGGCCAAGGGACCA 431

Qy        302 AGGTGGAAATCAAACG 317
              ||||||| ||||||||
Db        432 AGGTGGAGATCAAACG 447


RESULT 7
US-10-693-629-65
; Sequence 65, Application US/10693629
; Publication No. US20040120948A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;  APPLICANT:  MIKAYAMA, Toshifumi
;  APPLICANT:  YOSHIDA, Hitoshi
;  APPLICANT:  FORCE, Walker, R.
;  APPLICANT:  CHEN, Xingjie
;  APPLICANT:  TAKAHASHI, Nobuaki
;  TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
;  FILE REFERENCE: 021286-0306473
;  CURRENT APPLICATION NUMBER: US/10/693,629
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/13672
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US09/844,684
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: JP2001/142482
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: JP2001/310535
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: US10/040,244
;  PRIOR FILING DATE: 2001-10-26
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 728
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-693-629-65

  Query Match             88.3%;  Score 280.8;  DB 17;  Length 728;
  Best Local Similarity   93.0%;  Pred. No. 1.5e-83;
  Matches  294;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db        132 AGATGACCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGAGTCACCATCACTT 191

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        192 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 251

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||| |||||||||||||||||||||| ||||||||||
Db        252 CCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 311

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||
Db        312 GCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 371

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||| |||||||||     || || ||||| |||||||
Db        372 TTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTCGGCCAAGGGACCA 431

Qy        302 AGGTGGAAATCAAACG 317
              ||||||| ||||||||
Db        432 AGGTGGAGATCAAACG 447


RESULT 8
US-10-324-493-21
; Sequence 21, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
;  APPLICANT: Pluenneke, John
;  TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 3005-C
;  CURRENT APPLICATION NUMBER: US/10/324,493
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/847,816
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: 09/579,808
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/665,343
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/785,934
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(321)
US-10-324-493-21

  Query Match             88.2%;  Score 280.4;  DB 15;  Length 321;
  Best Local Similarity   93.3%;  Pred. No. 1.6e-83;
  Matches  293;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCACCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||| |||||||| | |||||| |||| |||||||
Db        248 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCATTCACTTTCGGCCCTGGGACCA 307

Qy        302 AGGTGGAAATCAAA 315
              | ||||| ||||||
Db        308 AAGTGGATATCAAA 321


RESULT 9
US-10-292-088-47
; Sequence 47, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 705
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-292-088-47

  Query Match             88.1%;  Score 280.2;  DB 13;  Length 705;
  Best Local Similarity   92.7%;  Pred. No. 2.3e-83;
  Matches  294;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||| |||||||||||||||||||||||| ||||
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Db         68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 127

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
Db        128 GTCGGGCGAGTCAGGGTATTTACAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
Db        188 CCCCTAACCTCCTGATCTATACTGCATCCACTTTACAAAGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
Db        248 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCTGAAGATT 307

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db        308 TTGCAACTTACTATTGTCAACAGGCTAACATTTTCCCGCTCACTTTCGGCGGAGGGACCA 367

Qy        302 AGGTGGAAATCAAACGA 318
Db        368 AGGTGGAGATCAAACGA 384

RESULT 10
US-10-269-711-28
; Sequence 28, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  DeVries, Peter J.
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Ostrow, Dave
;  APPLICANT:  Weiler, James
;  APPLICANT:  Green, Larry
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 6989.US.O1
;  CURRENT APPLICATION NUMBER: US/10/269,711
;  CURRENT FILING DATE:  2002-10-14
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-269-711-28

  Query Match             88.0%;  Score 279.8;  DB 12;  Length 322;
  Best Local Similarity   93.0%;  Pred. No. 2.5e-83;
  Matches  293;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
Db          8 AGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCTCCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
Db        128 CCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAACGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db        248 TTGCAACTTACTTTTGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
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Db        308 AAGTGGATATCAAAC 322

RESULT 11
US-10-041-860-85
; Sequence 85, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-041-860-85

  Query Match             88.0%;  Score 279.8;  DB 15;  Length 322;
  Best Local Similarity   93.0%;  Pred. No. 2.5e-83;
  Matches  293;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCATTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db        248 TTGCATCTTACTATTGTCAACAGTCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
Db        308 AGGTGGAGATCAAAC 322

RESULT 12
US-10-665-383-63
; Sequence 63, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
;  APPLICANT: Floege, Juergen
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Keyt, Bruce
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
;  TITLE OF INVENTION:  USING ANTI-PDGF-DD ANTIBODIES
;  FILE REFERENCE: ABGENIX.052A
;  CURRENT APPLICATION NUMBER: US/10/665,383
;  CURRENT FILING DATE:  2003-09-16
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;  PRIOR APPLICATION NUMBER: 60/411,137
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-665-383-63

  Query Match           88.0%;  Score 279.8;  DB 17;  Length 322;
  Best Local Similarity  93.0%;  Pred. No. 2.5e-83;
  Matches  293;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||| |||||||||||||||||| ||||||||||
Db        128 CCCCTAAGCTCCTGATCTATGCTGCATCCATTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||  |||||||||||||||| ||||||||||||    || ||  ||||| |||||||
Db        248 TTGCATCTTACTATTGTCAACAGTCTAACAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
              ||||||| |||||||
Db        308 AGGTGGAGATCAAAC 322


RESULT 13
US-10-292-088-19
; Sequence 19, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-292-088-19

  Query Match           87.7%;  Score 278.8;  DB 13;  Length 321;
  Best Local Similarity  93.0%;  Pred. No. 5.4e-83;
  Matches  292;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          8 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||  ||||||||| ||||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||| |||||||||||||||||| ||||||||||
Db        128 CCCCTAAACTCCTGATTTATTCTGCCTCCGGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              ||||||||||||||||||||||| || |||||||||||  |||||| |||   |||||||
Db        248 TTGCAACTTACTATTGTCAACAGACTGACAGTTTCCCGCTCACTTTCGGCGGCGGGACCA 307

Qy        302 AGGTGGAAATCAAA 315
              ||||||| ||||||
Db        308 AGGTGGAGATCAAA 321


RESULT 14
US-10-269-711-16
; Sequence 16, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  DeVries, Peter J.
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Ostrow, Dave
;  APPLICANT:  Weiler, James
;  APPLICANT:  Green, Larry
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 6989.US.O1
;  CURRENT APPLICATION NUMBER: US/10/269,711
;  CURRENT FILING DATE:  2002-10-14
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-269-711-16

  Query Match           87.5%;  Score 278.2;  DB 12;  Length 322;
  Best Local Similarity  92.7%;  Pred. No. 8.5e-83;
  Matches  292;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || || |||||||||||||||||||||||||||||||||||||||||||| |||| ||||
Db          8 AGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCTCCATCACTT 67

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db         68 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||  |||||  |||||| |||||||||||||||| |||||||||  |||||||||
Db        128 CCCCTACGCTCCTAATCTATGCTGCATCCAGTTTGCAACGTGGGGTCCCATCAAGGTTCA 187

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        188 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||  |||||||||||||||||||||||| | ||||||  |||  |||||||
Db        248 TTGCAACTTACTTTTGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCA 307

Qy        302 AGGTGGAAATCAAAC 316
              | |||||  |||||||
Db        308 AAGTGGATATCAAAC 322


RESULT 15
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US-09-844-684-13
; Sequence 13, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
;  APPLICANT: GEMINI SCIENCE, INC.
;  APPLICANT:  LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
;  TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
;  FILE REFERENCE: 21286/0276339
;  CURRENT APPLICATION NUMBER: US/09/844,684
;  CURRENT FILING DATE:  2001-04-27
;  PRIOR APPLICATION NUMBER: US 60/200,601
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 716
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-844-684-13

  Query Match             87.3%;  Score 277.6;  DB 9;  Length 716;
  Best Local Similarity   92.4%;  Pred. No. 1.7e-82;
  Matches  292;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||| |||||||||||||||||| ||||
Db        120 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGCAGGAGACAGAGTCACCATCACTT 179

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        180 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAACAGAAACCAGGGAAAG 239

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| ||| ||||||||||||||||||||||| ||||||||||
Db        240 CCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 299

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||| |||||||||||||| |||||||||| ||||||||||||||||||||
Db        300 GCGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCGGCAGCCTGCAGCCTGAAGATT 359

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||    || || ||||| |||||||
Db        360 TTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACGTTCGGCCAAGGGACCA 419

Qy        302 AGGTGGAAATCAAACG 317
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Db        420 AGGTGGAGATCAAACG 435


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GenCore version 5.1.6

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Run on: August 13, 2004, 00:21:37 ; Search time 44.9697 Seconds
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Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	291	91.5	388	3	US-09-042-353-358	Sequence 358, App
2	291	91.5	388	4	US-08-758-417A-206	Sequence 206, App
3	283.4	89.1	420	3	US-09-042-353-420	Sequence 420, App
4	283.4	89.1	420	4	US-08-758-417A-220	Sequence 220, App
5	283.4	89.1	3819	3	US-09-042-353-393	Sequence 393, App
6	283.4	89.1	3819	4	US-08-758-417A-243	Sequence 243, App
7	277	87.1	439	3	US-09-042-353-360	Sequence 360, App
8	277	87.1	439	4	US-08-758-417A-208	Sequence 208, App
9	275.4	86.6	384	1	US-08-259-372A-13	Sequence 13, Appl
10	275.4	86.6	384	1	US-08-468-671-13	Sequence 13, Appl
11	268.4	84.4	321	3	US-09-240-274-109	Sequence 109, App
12	266.8	83.9	321	3	US-09-240-274-199	Sequence 199, App
13	263.6	82.9	321	3	US-09-240-274-98	Sequence 98, Appl
14	263.6	82.9	321	3	US-09-240-274-102	Sequence 102, App
15	263.6	82.9	321	3	US-09-240-274-218	Sequence 218, App
16	263.6	82.9	321	3	US-09-240-274-221	Sequence 221, App
17	263.6	82.9	321	3	US-09-240-274-222	Sequence 222, App
18	262	82.4	321	3	US-09-240-274-215	Sequence 215, App
19	262	82.4	321	3	US-09-240-274-217	Sequence 217, App
20	260.4	81.9	321	3	US-09-240-274-113	Sequence 113, App
21	259.4	81.6	324	2	US-08-378-939-31	Sequence 31, Appl
22	259.4	81.6	324	2	US-08-378-939-33	Sequence 33, Appl
23	259.4	81.6	714	4	US-09-472-087-62	Sequence 62, Appl
24	258.8	81.4	321	3	US-09-240-274-107	Sequence 107, App
25	257.8	81.1	390	2	US-08-646-367-2	Sequence 2, Appli
26	257.2	80.9	321	3	US-09-240-274-105	Sequence 105, App
27	257.2	80.9	321	3	US-09-240-274-216	Sequence 216, App
28	257	80.8	324	3	US-09-240-274-206	Sequence 206, App
29	256.2	80.6	324	2	US-08-378-939-23	Sequence 23, Appl
30	255.6	80.4	321	3	US-09-240-274-104	Sequence 104, App
31	255.6	80.4	321	3	US-09-240-274-201	Sequence 201, App
32	255.6	80.4	321	3	US-09-240-274-211	Sequence 211, App
33	255.4	80.3	324	3	US-09-240-274-101	Sequence 101, App
34	255.4	80.3	324	3	US-09-240-274-112	Sequence 112, App
35	255.4	80.3	324	3	US-09-240-274-210	Sequence 210, App
36	254.6	80.1	324	2	US-08-378-939-17	Sequence 17, Appl
37	254	79.9	321	3	US-09-240-274-207	Sequence 207, App
38	253	79.6	324	2	US-08-378-939-15	Sequence 15, Appl
39	252.4	79.4	321	3	US-09-240-274-106	Sequence 106, App
40	252.2	79.3	324	3	US-09-240-274-224	Sequence 224, App
41	250.8	78.9	321	3	US-09-240-274-205	Sequence 205, App
42	250.6	78.8	324	3	US-09-240-274-110	Sequence 110, App
43	250.2	78.7	417	4	US-09-472-087-48	Sequence 48, Appl
44	250	78.6	321	3	US-08-599-226-36	Sequence 36, Appl
45	250	78.6	321	3	US-09-125-098-36	Sequence 36, Appl

ALIGNMENTS

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RESULT 1
US-09-042-353-358
; Sequence 358, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  358:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  388 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-358

  Query Match            91.5%;  Score 291;  DB 3;  Length 388;
  Best Local Similarity  95.2%;  Pred. No. 9.7e-90;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              ||||||| |||||||||||| |||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
              || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388


RESULT 2
US-08-758-417A-206
; Sequence 206, Application US/08758417A
; Patent No. 6300129
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;  GENERAL INFORMATION:
;       APPLICANT: Lonberg, Nils
;                  Kay, Robert M.
;       TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                           Producing Heterologous Antibodies
;       NUMBER OF SEQUENCES: 417
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 206:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 388 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

  Query Match            91.5%;  Score 291;  DB 4;  Length 388;
  Best Local Similarity  95.2%;  Pred. No. 9.7e-90;
  Matches  300;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||||
Db        134 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
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                ||||||| |||||||||||| |||||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
                |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
                |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        314 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAAC 316
                || |||| |||||||
Db        374 AGCTGGAGATCAAAC 388
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RESULT 3
US-09-042-353-420
; Sequence 420, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-042-353-420

Query Match 89.1%; Score 283.4; DB 3; Length 420;
Best Local Similarity 93.4%; Pred. No. 4e-87;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         80 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 139

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| |||||||| |||||||||||||||||| |||||||| ||||
Db        140 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||| ||||| ||||||||||
Db        200 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        260 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 379

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        380 AGCTGGAGATCAAACGA 396
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RESULT 4
US-08-758-417A-220
; Sequence 220, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:

```
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;          COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;          ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;          TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;      INFORMATION FOR SEQ ID NO: 220:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 420 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;          MOLECULE TYPE: DNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-758-417A-220

  Query Match             89.1%;  Score 283.4;  DB 4;  Length 420;
  Best Local Similarity   93.4%;  Pred. No. 4e-87;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         80 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 139

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||| ||||||||| |||||||||||||||||||| ||||||| ||||
Db        140 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 199

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||| ||||| ||||||||||
Db        200 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 259

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        260 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 319

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||
Db        320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 379

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        380 AGCTGGAGATCAAACGA 396


RESULT 5
US-09-042-353-393
; Sequence 393, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
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;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  393:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3819 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-393

  Query Match             89.1%;  Score 283.4;  DB 3;  Length 3819;
  Best Local Similarity   93.4%;  Pred. No. 1.1e-86;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2513 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 2572

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| |||||||| ||||
Db       2573 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 2632

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db       2633 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 2692

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       2693 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 2752

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||
Db       2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 2812

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db       2813 AGCTGGAGATCAAACGA 2829


RESULT 6
US-08-758-417A-243
; Sequence 243, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;        APPLICANT: Lonberg, Nils
;                   Kay, Robert M.
;        TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                            Producing Heterologous Antibodies
;        NUMBER OF SEQUENCES: 417
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/758,417A
;             FILING DATE: 02-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/728,463
;             FILING DATE: 10-OCT-1996
;             APPLICATION NUMBER: US 08/544,404
;             FILING DATE: 10-OCT-1995
;             APPLICATION NUMBER: US 08/352,322
;             FILING DATE: 07-DEC-1994
;             APPLICATION NUMBER: US 08/209,741
;             FILING DATE: 09-MAR-1994
;             APPLICATION NUMBER: US 08/165,699
;             FILING DATE: 10-DEC-1993
;             APPLICATION NUMBER: US 08/161,739
;             FILING DATE: 03-DEC-1993
;             APPLICATION NUMBER: US 08/155,301
;             FILING DATE: 18-NOV-1993
;             APPLICATION NUMBER: US 08/096,762
;             FILING DATE: 22-JUL-1993
;             APPLICATION NUMBER: US 08/053,131
;             FILING DATE: 26-APR-1993
;             APPLICATION NUMBER: US 07/990,860
;             FILING DATE: 16-DEC-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Serafini, Andrew T.
;             REGISTRATION NUMBER: 41,303
;             REFERENCE/DOCKET NUMBER: 014643-009030US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 243:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3819 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243

  Query Match             89.1%;  Score 283.4;  DB 4;  Length 3819;
  Best Local Similarity   93.4%;  Pred. No. 1.1e-86;
  Matches  296;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2513 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 2572

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||| |||||||| |||||||||||||||||||| |||||||| ||||
Db       2573 GTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAG 2632

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              | ||||| |||||||||||| |||||||||||||||||||||| ||||| ||||||||||
Db       2633 CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCAAGGTTCA 2692

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       2693 GCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 2752

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||
Db       2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCA 2812

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db       2813 AGCTGGAGATCAAACGA 2829
```

```
RESULT 7
US-09-042-353-360
; Sequence 360, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  360:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  439 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-360

  Query Match             87.1%;  Score 277;  DB 3;  Length 439;
  Best Local Similarity   92.1%;  Pred. No. 6.2e-85;
  Matches  292;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||| ||  ||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db        134 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||   ||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||||||| || || |||||  | | |||| ||||||||||||||||||||||||||
Db        314 TTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        374 AGCTGGAGATCAAACGA 390


RESULT 8
US-08-758-417A-208
; Sequence 208, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;        APPLICANT: Lonberg, Nils
;                   Kay, Robert M.
;        TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                            Producing Heterologous Antibodies
;        NUMBER OF SEQUENCES: 417
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/758,417A
;             FILING DATE: 02-Dec-1996
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;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 208:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 439 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-08-758-417A-208

  Query Match           87.1%;  Score 277;  DB 4;  Length 439;
  Best Local Similarity  92.1%;  Pred. No. 6.2e-85;
  Matches  292;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||| ||  ||||||||||||||||||||||||||||||| ||||
Db         74 AGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 133

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              |||||||||||||||||||||||| |||||||||||||||||||||||| |||||
Db        134 GTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAG 193

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||   ||||||||||||||||||||||||||||||||| ||||||||||
Db        194 CCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        254 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 313

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
               ||||||||| || || ||||||  | | |||| ||||||||||||||||||||||||
Db        314 TTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCA 373

Qy        302 AGGTGGAAATCAAACGA 318
              || |||| |||||||||
Db        374 AGCTGGAGATCAAACGA 390


RESULT 9
US-08-259-372A-13
; Sequence 13, Application US/08259372A
; Patent No. 5565354
;  GENERAL INFORMATION:
;    APPLICANT:  Ostberg, Lars G.
;    TITLE OF INVENTION:  PRODUCTION OF HUMAN MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/259,372A
;      FILING DATE:  14-JUN-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/871,426
;      FILING DATE:  21-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/676,036
;      FILING DATE:  27-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/538,796
;      FILING DATE:  15-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/192,754
;      FILING DATE:  11-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/925,196
;      FILING DATE:  31-OCT-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/904,517
;      FILING DATE:  05-SEP-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-50-7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  384 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Hybridoma
;      CELL LINE:  ZM1-2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..384
US-08-259-372A-13

  Query Match           86.6%;  Score 275.4;  DB 1;  Length 384;
  Best Local Similarity  91.8%;  Pred. No. 2.1e-84;
  Matches  291;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || |||||||||||||||||||||||||||||||| |||||||||||||| | ||||
Db         68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTGGGAGACAGAGTCACCGTCACTT 127

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        128 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||||||||||||| || ||||||||||||||||||||||||||| ||||||||||
Db        188 CCCCTAAACTCCTGATCCATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||| |||||||||| |||||||||| ||||||||||
Db        248 TCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGCCTGCAGGCTGAAGATT 307

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||| |||||||||||||||||| ||||| |||| |  ||||| |||   |||||||
Db        308 TTGCAACCTACTATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTCGGCGGAGGGACCA 367

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||  ||||||||
Db        368 AGGTGGACTTCAAACGA 384
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RESULT 10
US-08-468-671-13
; Sequence 13, Application US/08468671
; Patent No. 5648077
;  GENERAL INFORMATION:
;    APPLICANT:  Ostberg, Lars G.
;    TITLE OF INVENTION:  PRODUCTION OF HUMAN MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,671
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/259,372
;      FILING DATE:  14-JUN-1994
;      APPLICATION NUMBER:  US 07/871,426
;      FILING DATE:  21-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/676,036
;      FILING DATE:  27-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/538,796
;      FILING DATE:  15-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/192,754
;      FILING DATE:  11-MAY-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/925,196
;      FILING DATE:  31-OCT-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/904,517
;      FILING DATE:  05-SEP-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-50-7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  384 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Hybridoma
;      CELL LINE:  ZM1-2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..384
US-08-468-671-13

  Query Match             86.6%;  Score 275.4;  DB 1;  Length 384;
  Best Local Similarity   91.8%;  Pred. No. 2.1e-84;
  Matches  291;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 AGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACTT 61
              || | || ||||||||||||||||||||||||||||||| ||||||||||||||| | ||||
Db         68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTGGGAGACAGAGTCACCGTCACTT 127

Qy         62 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 187

Qy        122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCA 181
              |||||||||||||||||| || ||||||||||||||||||||||||||| ||||||||||
Db        188 CCCCTAAACTCCTGATCCATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 247

Qy        182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
              ||||||||||||||||||||||||| |||||||||| |||||||||| ||||||||||
Db        248 TCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGCCTGCAGGCTGAAGATT 307

Qy        242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
              |||||| |||||||||||||||||| ||||| |||| |  ||||| |||   |||||||
Db        308 TTGCAACCTACTATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTCGGCGGAGGGACCA 367

Qy        302 AGGTGGAAATCAAACGA 318
              |||||||  ||||||||
Db        368 AGGTGGACTTCAAACGA 384
```

```
RESULT 11
US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-109

  Query Match             84.4%;  Score 268.4;  DB 3;  Length 321;
  Best Local Similarity   90.3%;  Pred. No. 4.7e-82;
  Matches  287;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;
```

```
Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              ||||||| |||||||||| ||| ||||||||||||||||||||||||||||||||| |||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              || ||||| |||||| | |||||||| |  |||   ||||||||||||||||||||||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              |||||||| |||||||||||| ||||||||||||||||||||||||||| |||||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              || |||||||||||||||||||||| || |||||||||||||| ||||| |||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTCCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              | |||||||||| || |||||||||  ||| |||| ||||||||||||||||||||||||
Db        244 TTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCGTACACTTTTGGCCAGGGGACC 303

Qy        301 AAGGTGGAAATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAGCTGGAGATCAAACGA 321
```

RESULT 12
US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

Query Match 83.9%; Score 266.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 1.6e-81;
Matches 286; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              ||||||| |||||||||| ||| ||||||||||||||||||||||||||||||||| |||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              || ||||| |||||| | |||||||| |  |||   ||||||||||||||||||||||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              |||||||| |||||||||||| ||||||||||||||| |||||||||| |||||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              || |||||||||||||||||||||| |||||||||||||| ||||| |||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              | |||||||||||| |||||||||  | |||||  ||| |||||||||||||||||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGACC 303

Qy        301 AAGGTGGAAATCAAACGA 318
              ||| |||| |||||||||
Db        304 AAGCTGGAGATCAAACGA 321
```

RESULT 13
US-09-240-274-98
; Sequence 98, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-98

Query Match 82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 2e-80;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              ||||||| |||||||||| ||| ||||||||||||||||||||||||||||||||| |||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              || ||||| |||||||| |||| | |  |||| ||||||||||||||||||||||||||
Db         64 TGCCGGGCAAGTCAGGGCTTTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              |||||||| | |||||||||| || |||||||||||||||||||||||| |||||||||
Db        124 GCCCCTAAGCGCCTGATCTATGCTACATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              |||||||||||||||||||||| |||| |||||| |||| ||||||||||||||||||||
Db        184 AGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAACAGCCTGCAGCCTGAAGAT 243

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              |||||||||||| || |||| |||| ||| ||||||||||  || || |||||  |||||
Db        244 TCTGCAACTTATTACTGTCTACAGCATAATAGTTTCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        304 AAGGTGGAAATCAAACGA 321
```

RESULT 14
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380

```
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

  Query Match             82.9%;  Score 263.6;  DB 3;  Length 321;
  Best Local Similarity   89.3%;  Pred. No. 2e-80;
  Matches  284;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              |||||||| |||||||||||| ||| ||||||||||||||||||||||||||||||| |||
Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT 63

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              || ||||| |||||| | |||||||| |   |||   ||||||||||||||||||||||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              |||||||| |||||||||||| ||||||||||||||||||||||||| |||||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              || |||||||||||||||||||||||| |||||||||||||| ||||| |||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              | |||||||||||| |||||||||  | |||||  || ||  || || ||||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        304 AAGGTGGAAATCAAACGA 321


RESULT 15
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

  Query Match             82.9%;  Score 263.6;  DB 3;  Length 321;
  Best Local Similarity   89.3%;  Pred. No. 2e-80;
  Matches  284;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 GAGCTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATAACT 60
              |||||||| |||||||||||| ||| |||||||||||||||||||||||||||||| | |||

Db          4 GAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCACT 63

Qy         61 TGTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA 120
              || ||||| |||||| | |||||||| |   |||   ||||||||||||||||||||||||
Db         64 TGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAA 123

Qy        121 GCCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTC 180
              |||||||| |||||||||||| ||||||||||||||||||||||||| |||||||||
Db        124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTC 183

Qy        181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
              || |||||||||||||||||||||||| |||||||||||||| ||||| |||||||||
Db        184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243

Qy        241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
              | |||||||||||| |||||||||  | |||||  |||||  || || ||||| ||||||
Db        244 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGACC 303

Qy        301 AAGGTGGAAATCAAACGA 318
              ||||||||||||||||||
Db        304 AAGGTGGAAATCAAACGA 321


Search completed: August 13, 2004, 07:18:10
Job time : 44.9697 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 10.0182 Seconds
(without alignments)
1094.593 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	479.5	78.7	116	2	S37456	Ig mu chain - huma
2	476.5	78.2	135	2	S78051	Ig heavy chain pre
3	475.5	78.1	128	2	S31514	Ig heavy chain - h
4	465	76.4	122	2	S69912	Ig V-D-J region (N
5	464.5	76.3	147	2	S13519	Ig heavy chain V r
6	460	75.5	130	2	S30534	Ig heavy chain V r
7	458.5	75.3	140	2	I37782	Ig variable region
8	453	74.4	99	2	S26801	Ig heavy chain V r
9	452.5	74.3	146	2	S09710	Ig heavy chain V r
10	451.5	74.1	121	2	S44113	Ig heavy chain V r
11	451.5	74.1	130	2	S31690	Ig heavy chain V r
12	450.5	74.0	127	2	S19668	Ig heavy chain V r
13	450.5	74.0	146	2	S09711	Ig heavy chain V r
14	449.5	73.8	155	2	S31511	Ig heavy chain - h
15	446.5	73.3	155	2	S31512	Ig heavy chain - h
16	444	72.9	137	2	S31676	Ig heavy chain V r
17	440	72.2	139	2	S31586	Ig heavy chain V r
18	439	72.1	145	2	S78055	Ig heavy chain pre
19	436	71.6	99	2	S26803	Ig heavy chain V r
20	435.5	71.5	123	2	S30530	Ig heavy chain V r
21	434	71.3	129	2	S44114	Ig heavy chain V r
22	433.5	71.2	117	2	E34964	Ig heavy chain pre
23	432.5	71.0	109	2	PH1673	Ig heavy chain V r
24	431	70.8	99	2	S26802	Ig heavy chain V r
25	430	70.6	97	2	PL0118	Ig heavy chain V-I
26	430	70.6	99	2	S26899	Ig heavy chain V r
27	427	70.1	110	2	S44110	Ig heavy chain V-D
28	426	70.0	139	2	A41287	Ig heavy chain pre
29	425.5	69.9	121	2	C55257	Ig gamma heavy cha
30	424	69.6	118	2	A26340	Ig heavy chain pre
31	423	69.5	118	2	S20780	Ig heavy chain V r
32	421.5	69.2	140	2	A49045	Ig heavy chain V r
33	419.5	68.9	129	1	D2HUWA	Ig heavy chain V-I
34	419	68.8	135	2	S31604	Ig heavy chain V r
35	418.5	68.7	132	2	A38911	Ig heavy chain V r
36	418	68.6	99	2	S26807	Ig heavy chain V r
37	417	68.5	115	2	S57464	Ig heavy chain V-J
38	417	68.5	126	2	S47010	Ig heavy chain V4.
39	417	68.5	140	2	S78052	Ig heavy chain pre
40	416.5	68.4	140	2	A24770	hypothetical hybri
41	415.5	68.2	143	2	B49028	Ig heavy chain V-I
42	415	68.1	99	2	S12418	Ig heavy chain V r
43	414.5	68.1	137	2	S31585	Ig heavy chain V r
44	414	68.0	120	2	PT0370	Ig mu chain precur
45	412.5	67.7	98	2	S26902	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S37456
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 479.5; DB 2; Length 116;
Best Local Similarity 76.1%; Pred. No. 4.6e-38;
Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

```
Qy          6 GLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKSRI 65
              |||||:|||||:| |||||| ||||||||||||||||||||||:||:||||||||||:
Db          1 GLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRV 60

Qy         66 AMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYT--------LDIWGQGTLVTVSS 114
                :|||||:|:|||:|:|||||||||||||||  ||:        :|:||:|| |||||
Db         61 TISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGYSYGYYYYYYYMDVWGKGTTVTVSS 116
```

RESULT 2
S78051
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78051; S23716
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Molecule type: mRNA
A;Residues: 1-135 <HAR>
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23716
A;Molecule type: mRNA

```
A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

  Query Match             78.2%;  Score 476.5;  DB 2;  Length 135;
  Best Local Similarity   76.3%;  Pred. No. 1e-37;
  Matches   90;  Conservative   13;  Mismatches   10;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| ||||||  | :|| |||| |||||||||| ||:|||||:||||
Db         18 ESGPGLVKPSETLSLTCTVSGGSISRGSHYWGWIRQPPGKGLEWIGSIYYSGNTYFNPSL 77

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL--DGYTL---DIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||||  | |||    |:|||||:|||||
Db         78 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGTTVTVSS 135


RESULT 3
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

  Query Match             78.1%;  Score 475.5;  DB 2;  Length 128;
  Best Local Similarity   76.7%;  Pred. No. 1.2e-37;
  Matches   89;  Conservative   10;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||:|:|||||:| |||||| |||:|||||||||  |||| :|| ||:||||| |
Db         13 ESGPGLVRPSQTLSLTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIYFSGSTYYNPFL 72

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD---GYTLDIWGQGTLVTVSS 114
              |||: :|||||||:|||||  ||| ||||||||||:    ||   | ||||||||||
Db         73 KSRVIISVDTSENQFSLRLTSVTPADTAVYYCARIGYNFGYGFDPWGQGTLVTVSS 128


RESULT 4
S69912
Ig V-D-J region (ND) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69912
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: EMBL:Z33398; NID:g871347; PIDN:CAA83849.1; PID:g887460
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             76.4%;  Score 465;  DB 2;  Length 122;
  Best Local Similarity   75.2%;  Pred. No. 1.1e-36;
  Matches   88;  Conservative   14;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:|:|||||| | |::|:|||||||||||||| || ||::||||||
Db          6 ESGPGLVKPSQTLSLTCSVSGGSISSDGHFWNWIRQHPGKGLEWIGNIYFSGSSYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR----LDGYTLDIWGQGTLVTVSS 114
              ||||::|||||:|:|||||  ||||||||||:|||       | || ||||||| :||
Db         66 KSRISISVDTSKNQFSLRLKSVTAADTAVYFCARGFFFRGTYGLDTWGQGTLVRLSS 122


RESULT 5
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

  Query Match             76.3%;  Score 464.5;  DB 2;  Length 147;
  Best Local Similarity   75.9%;  Pred. No. 1.5e-36;
  Matches   88;  Conservative   11;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||| |||| |||||||||| ||:||:|||||||
Db         32 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 91

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR---LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||      |   | ||||||||||||
Db         92 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPLLWFGELFDYWGQGTLVTVSS 147


RESULT 6
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             75.5%;  Score 460;  DB 2;  Length 130;
  Best Local Similarity   72.8%;  Pred. No. 3.5e-36;
  Matches   91;  Conservative   10;  Mismatches   12;  Indels   12;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| || |||||||| |||||||| || ||:| |||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG------YT------LDIWGQGTL 109
              |||: :|||||:|:|||:|:|||||||||||||||  |      ||       |||||||:
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIWGQGTM 125
```

```
Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130
```

RESULT 7
I37782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

```
  Query Match             75.3%;  Score 458.5;  DB 2;  Length 140;
  Best Local Similarity   75.4%;  Pred. No. 5.3e-36;
  Matches   89;  Conservative   12;  Mismatches   10;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| ||||||||||||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD-----GYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| :     |   | ||||||||||
Db         83 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTLVTVSS 140
```

RESULT 8
S26801
Ig heavy chain V region (DP-65) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Accession: S26801; S26900
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26801
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WEN>
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <TOM>
A;Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

```
  Query Match             74.4%;  Score 453;  DB 2;  Length 99;
  Best Local Similarity   86.2%;  Pred. No. 1.2e-35;
  Matches   81;  Conservative   10;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR 95
              |||: :|||||:|:|||:|:|||||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 99
```

RESULT 9
S09710
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S09710
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09710
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

```
  Query Match             74.3%;  Score 452.5;  DB 2;  Length 146;
  Best Local Similarity   68.3%;  Pred. No. 2e-35;
  Matches   84;  Conservative   16;  Mismatches   12;  Indels   11;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:|:|||||: ||| || |:|| |||||||||  |::||:|||||||
Db         25 ESGPGLVKPSETLSLTCSVSGGSVSSGGLYWGWVRQPPGKGLEWIGSIFYSGSTYYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGY----------TLDIWGQGTLVT 111
              |||: :|||| :| |||:|:||||||||||||| |  ||          :|:||||| ||
Db         85 KSRVTISVDTLKNNFSLKLSSVTAADTAVYYCTR-PGYGDTSVRKRVWNMDLWGQGTTVT 143

Qy        112 VSS 114
              |||
Db        144 VSS 146
```

RESULT 10
S44113
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <HAW>
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

```
  Query Match             74.1%;  Score 451.5;  DB 2;  Length 121;
  Best Local Similarity   73.3%;  Pred. No. 2e-35;
  Matches   85;  Conservative   13;  Mismatches   15;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||| | |  ||| | || |||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YT-LDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||| ||||:|| |  |:  | | |||||||||
Db         66 KSRVTLSVDTSKNQFSLKLSSVTAADTGVYYCSRLSGGYYSDFDYWSQGTLVTVSS 121
```

```
RESULT 11
S31690
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

  Query Match             74.1%;  Score 451.5;  DB 2;  Length 130;
  Best Local Similarity   72.1%;  Pred. No. 2.2e-35;
  Matches   88;  Conservative   11;  Mismatches   12;  Indels   11;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||||| || ||||||||||||:||:| |||||
Db         11 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWSRQPPGKGLEWIGYIYYSGSTNYNPSL 68

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG---------YTLDIWGQGTLVTV 112
              |||: :|||||:|:|||:|:|||||||||||||              |  | |||||||||
Db         69 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSSVLLWFGELLYYFDYWGQGTLVTV 128

Qy        113 SS 114
              ||
Db        129 SS 130


RESULT 12
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118,'E',120-121,'T',123-126,'F' <JON>
A;Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             74.0%;  Score 450.5;  DB 2;  Length 127;
  Best Local Similarity   69.7%;  Pred. No. 2.7e-35;
  Matches   85;  Conservative   15;  Mismatches   13;  Indels    9;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              :|| |||||:|||||:|:||| || |||| ||||||  |||||||| ::||| |||||||
Db          6 QSGSGLVKPSQTLSLTCSVSGDSISSGGYSWSWIRQPSGKGLEWIGSVHHSGPTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG---------YTLDIWGQGTLVTV 112
              |||: |||||:|:|||:| |||||||||:|:|||  |          | :|:||:||||||
Db         66 KSRVTMSVDTSKNQFSLKLKSVTAADTAMYFCAREGGSTWRSLYKHYYMDVWGKGTLVTV 125

Qy        113 SS 114
              ||
Db        126 SS 127


RESULT 13
S09711
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

  Query Match             74.0%;  Score 450.5;  DB 2;  Length 146;
  Best Local Similarity   68.0%;  Pred. No. 3.1e-35;
  Matches   83;  Conservative   17;  Mismatches   13;  Indels    9;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::|||::| |||||: | | ||||||| |||| |||||||:||:| |||||
Db         25 ESGPGLVKPSETLSVTCTVSGGSVSSSGLYWSWIRQPPGKGPEWIGYIYYSGSTNYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL---------DGYTLDIWGQGTLVTV 112
              :||: :|||||:|:|||:| |||||||||||||:          | :|:||:|| |||
Db         85 RSRVTISVDTSKNQFSLKLGSVTAADTAVYYCARVLVSRTSISQYSYYMDVWGKGTTVTV 144

Qy        113 SS 114
              ||
Db        145 SS 146


RESULT 14
S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A;Reference number: S31509
A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

  Query Match             73.8%;  Score 449.5;  DB 2;  Length 155;
  Best Local Similarity   70.8%;  Pred. No. 4.1e-35;
  Matches   85;  Conservative   15;  Mismatches   11;  Indels    9;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| ||||||||||||::|:  ||| |
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPL 95

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-------LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:::|||||||||||||        | | :|:||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTVTVSS 155


RESULT 15
```

S31512
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 446.5; DB 2; Length 155;
Best Local Similarity 70.0%; Pred. No. 7.8e-35;
Matches 84; Conservative 16; Mismatches 11; Indels 9; Gaps 2;

```
Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| ||||||||||||::|:  ||| :
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPI 95

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG-------YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|:||::::|||||||||||||  |       | :|:|||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYVYYGMDVWGQGTTVTVSS 155
```

Search completed: August 8, 2004, 12:18:53
Job time : 10.0182 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 6.21818 Seconds
(without alignments)
954.620 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	419.5	68.9	129	1	HV2F_HUMAN	P01824 homo sapien
2	405	66.5	146	1	HV2I_HUMAN	P06331 homo sapien
3	374.5	61.5	137	1	HV46_MOUSE	P01822 mus musculu
4	369.5	60.7	117	1	HV2G_HUMAN	P01825 homo sapien
5	361.5	59.4	113	1	HV47_MOUSE	P01823 mus musculu
6	342.5	56.2	116	1	HV61_MOUSE	P18532 mus musculu
7	341.5	56.1	116	1	HV60_MOUSE	P18531 mus musculu
8	334	54.8	117	1	HV62_MOUSE	P18533 mus musculu
9	321.5	52.8	144	1	HV43_MOUSE	P01819 mus musculu
10	304	49.9	135	1	HV02_XENLA	P20957 xenopus lae
11	300	49.3	120	1	HV2B_HUMAN	P01815 homo sapien
12	295	48.4	119	1	HV40_MOUSE	P01810 mus musculu
13	293	48.1	122	1	HV3A_HUMAN	P01762 homo sapien
14	288	47.3	119	1	HV38_MOUSE	P01808 mus musculu
15	285.5	46.9	119	1	HV2C_HUMAN	P01816 homo sapien
16	285	46.8	119	1	HV37_MOUSE	P01807 mus musculu
17	282.5	46.4	121	1	HV3J_HUMAN	P01771 homo sapien
18	280.5	46.1	117	1	HV2B_RABIT	P01828 oryctolagus
19	278.5	45.7	125	1	HV2D_HUMAN	P01817 homo sapien
20	276	45.3	114	1	HV3B_HUMAN	P01763 homo sapien
21	275	45.2	122	1	HV3G_HUMAN	P01768 homo sapien
22	274.5	45.1	121	1	HV2E_HUMAN	P01818 homo sapien
23	274	45.0	116	1	HV05_CARAU	P19181 carassius a
24	273	44.8	122	1	HV3H_HUMAN	P01769 homo sapien
25	272	44.7	114	1	HV2A_RABIT	P01827 oryctolagus
26	272	44.7	122	1	HV21_MOUSE	P01790 mus musculu
27	271	44.5	147	1	HV2H_HUMAN	P04438 homo sapien
28	270.5	44.4	115	1	HV3F_HUMAN	P01767 homo sapien
29	270.5	44.4	117	1	HV41_MOUSE	P01811 mus musculu
30	270	44.3	115	1	HV44_MOUSE	P01820 mus musculu
31	270	44.3	122	1	HV20_MOUSE	P01789 mus musculu
32	269.5	44.3	142	1	HV01_RAT	P01805 rattus norv
33	268.5	44.1	115	1	HV3D_HUMAN	P01765 homo sapien
34	268.5	44.1	117	1	HV42_MOUSE	P01812 mus musculu
35	267.5	43.9	117	1	HV12_MOUSE	P01756 mus musculu
36	267.5	43.9	123	1	HV25_MOUSE	P01794 mus musculu
37	267	43.8	116	1	HV45_MOUSE	P01821 mus musculu
38	267	43.8	126	1	HV2A_HUMAN	P01814 homo sapien
39	267	43.8	139	1	HV07_MOUSE	P01751 mus musculu
40	266.5	43.8	117	1	HV13_MOUSE	P01757 mus musculu
41	266.5	43.8	118	1	HV39_MOUSE	P01809 mus musculu
42	266.5	43.8	123	1	HV22_MOUSE	P01791 mus musculu
43	265.5	43.6	123	1	HV18_MOUSE	P01787 mus musculu
44	265.5	43.6	123	1	HV19_MOUSE	P01788 mus musculu
45	264.5	43.4	123	1	HV24_MOUSE	P01793 mus musculu

ALIGNMENTS

RESULT 1
HV2F_HUMAN
ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01825; 7FAB.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 68.9%; Score 419.5; DB 1; Length 129;
Best Local Similarity 62.7%; Pred. No. 5.8e-38;
Matches 79; Conservative 16; Mismatches 16; Indels 15; Gaps 2;

```
Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||| ||  |||| |||| |||||||||  :|::|: ||||||
Db          6 ESGPGLVKPSETLSLTCIVSGGPIRRTGYYWGWIRQPPGKGLEWIGGVYYTGSIYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR------------LDGYTLDIWGQGT 108
              : |: :|||||  |:||| | |::|||||:|||||              ||  :|:|||||
Db         66 RGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYYDIGTGSDDG--IDVWGQGT 123

Qy        109 LVTVSS 114
               | |||
Db        124 TVHVSS 129
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RESULT 2

```
HV2I_HUMAN
ID   HV2I_HUMAN     STANDARD;      PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146       IG HEAVY CHAIN V-II REGION ARH-77.
FT   DOMAIN       20    117       V SEGMENT.
FT   DOMAIN      118    127       D SEGMENT.
FT   DOMAIN      128    146       J SEGMENT.
FT   DISULFID     42    115       BY SIMILARITY.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16228 MW;  8D7FD52BB218171F CRC64;

  Query Match             66.5%;  Score 405;  DB 1;  Length 146;
  Best Local Similarity   66.9%;  Pred. No. 2.4e-36;
  Matches   81;  Conservative   13;  Mismatches   15;  Indels   12;  Gaps    3;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | |||||::||||:||| |||     |||||||| ||:|||||| | |||:| |  ||||
Db         28 GAGLVKPSETLSLTCAVFGGSF--SGYYWSWIRQPPGRGLEWIGEINHSGSTNYKTSLKS 85

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDG--------YTLDIWGQGTLVTVS 113
              |: :|:|||:| |||:|:|||||||||||||  | |        | :|:|||||  ||||
Db         86 RVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWNDVDYYYGMDVWGQGTTVTVS 145

Qy        114 S 114
              |
Db        146 S 146


RESULT 3
HV46_MOUSE
ID   HV46_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89238351; PubMed=2497341;
RA   Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT   "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT   gene segment.";
RL   Mol. Immunol. 26:431-434(1989).
RN   [2]
RP   SEQUENCE OF 1-31.
RX   MEDLINE=78094475; PubMed=414225;
RA   Jilka R.L., Pestka S.;
RT   "Amino acid sequence of the precursor region of MOPC-315 mouse
RT   immunoglobulin heavy chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN   [3]
RP   SEQUENCE OF 1-21.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [4]
RP   SEQUENCE OF 19-136.
RX   MEDLINE=74170779; PubMed=4524622;
RA   Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT   "Amino-acid sequence of the variable region of the heavy (alpha)
RT   chain of a mouse myeloma protein with anti-hapten activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN   [5]
RP   REVISION TO 53.
RX   MEDLINE=77244979; PubMed=268248;
RA   Hood L., Margolies M.N., Givol D., Zakut R.;
RL   Unpublished results, cited by:
RL   Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL   Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC   -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M27638; AAA61337.1; -.
DR   EMBL; X07880; CAA30727.1; -.
DR   PIR; PL0102; AVMS35.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    137       IG HEAVY CHAIN V REGION MOPC 315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DOMAIN      117    126       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      127    137       FRAMEWORK-4.
FT   DISULFID     40    114       BY SIMILARITY.
FT   CONFLICT     15     15       G -> GG (IN REF. 1; CAA30727).
FT   CONFLICT     15     15       G -> H (IN REF. 2).
FT   CONFLICT     77     78       GY -> YG (IN REF. 4).
FT   CONFLICT    102    102       N -> D (IN REF. 4).
FT   CONFLICT    123    123       MISSING (IN REF. 4).
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15399 MW;  FB3828304C2B81DC CRC64;

  Query Match             61.5%;  Score 374.5;  DB 1;  Length 137;
  Best Local Similarity   61.7%;  Pred. No. 4.1e-33;
  Matches   71;  Conservative   20;  Mismatches   21;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|:|||:|:|:| || | ||:|:|||| ||  |||:|:| : |:  |||||
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Db          24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYFWNWIRQFPGNKLEWLGFIKYDGSNGYNPSL 82

Qy          62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YTLDIWGQGTLVTVSS 114
               |:|:::: |||||:| |:||||| ||| |||| :  | | ||||| :|||| 
Db          83 KNRVSITRDTSENQFFLKLNSVTTEDTATYYCAGDNDHLYYFDYWGQGTTLTVSS 137


RESULT 4
HV2G_HUMAN
ID   HV2G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01825;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region NEWM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77242302; PubMed=407927;
RA   Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT   "Amino acid sequence of the VH region of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 16:3412-3420(1977).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX   MEDLINE=78066916; PubMed=618887;
RA   Saul F.A., Amzel L.M., Poljak R.J.;
RT   "Preliminary refinement and structural analysis of the Fab fragment
RT   from human immunoglobulin new at 2.0-A resolution.";
RL   J. Biol. Chem. 253:585-597(1978).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90404; G1HUNM.
DR   PDB; 7FAB; 31-JAN-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    111       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   TURN         30     31
FT   STRAND       33     39
FT   TURN         41     42
FT   STRAND       46     51
FT   TURN         53     54
FT   STRAND       57     59
FT   HELIX        61     63
FT   TURN         64     66
FT   STRAND       67     72
FT   TURN         73     76
FT   STRAND       77     82
FT   HELIX        87     89
FT   STRAND       91     98
FT   STRAND      104    107
FT   STRAND      111    115
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12790 MW;  2DA47B509562D237 CRC64;

  Query Match             60.7%;  Score 369.5;  DB 1;  Length 117;
  Best Local Similarity   61.4%;  Pred. No. 1.2e-32;
  Matches   70;  Conservative   22;  Mismatches   19;  Indels    3;  Gaps    2;

Qy           2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
               :||||||:|:|||||:| ||| :  :    |::|:|| ||:|||||||::: | :     |
Db           6 QSGPGLVRPSQTLSLTCTVSGSTFSND--YYTWVRQPPGRGLEWIGYVFYHGTSDDTTPL 63

Qy          62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-LDGYTLDIWGQGTLVTVSS 114
               :||: | ||||:|:|||||:|||||||||||||| |    :|:||||:||||| 
Db          64 RSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLIAGCIDVWGQGSLVTVSS 117


RESULT 5
HV47_MOUSE
ID   HV47_MOUSE     STANDARD;      PRT;   113 AA.
AC   P01823;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-60.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=84024551; PubMed=6414509;
RA   Juszczak E.C., Margolies M.N.;
RT   "Amino acid sequence of the heavy chain variable region from the A/J
RT   mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
RT   idiotype.";
RL   Biochemistry 22:4291-4296(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC       MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC       IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC       STRAIN A/J MICE.
DR   PIR; A02098; G2MS60.
DR   PDB; 1J1O; 18-FEB-03.
DR   PDB; 1J1P; 18-FEB-03.
DR   PDB; 1J1X; 18-FEB-03.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12734 MW;  38DC0E0E3F5075B7 CRC64;

  Query Match             59.4%;  Score 361.5;  DB 1;  Length 113;
  Best Local Similarity   62.8%;  Pred. No. 8.1e-32;
  Matches   71;  Conservative   18;  Mismatches   19;  Indels    5;  Gaps    2;

Qy           2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
               |||| ||||:|||||:|:|:| || |   ||:|||: ||  || :||| :||:|||||||
Db           6 ESGPSLVKPSQTLSLTCSVTGDSITSD--YWNWIRKFPGNKLEHMGYISYSGSTYYNPSL 63

Qy          62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
               |||:::: |||:|:: |:||||||: ||| |||  |       ||||||||||: 
Db          64 KSRISITRDTSKNQYYLQLNSVTSEDTATYYCTSL---RFAYWGQGTLVTVSA 113


RESULT 6
HV61_MOUSE
ID   HV61_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18532;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR   PIR; JT0508; HVMS1B.
DR   PDB; 1KCS; 11-MAY-02.
DR   PDB; 1KCV; 11-MAY-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION 1B43.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13158 MW;  1CB547253681FF74 CRC64;

  Query Match             56.2%;  Score 342.5;  DB 1;  Length 116;
  Best Local Similarity   69.1%;  Pred. No. 9.1e-30;
  Matches   65;  Conservative   13;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| ||||:|:|||:| |:| || | || | |||| ||  |||:|||::|||| |||||
Db         24 ESGPDLVKPSQSLSLTCTVTGYSITS-GYSWHWIRQFPGNKLEWMGYIHYSGNTSYNPSL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR 95
              ||||::: |||:|:| |:||||  ||| |||||
Db         83 KSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR 116


RESULT 7
HV60_MOUSE
ID   HV60_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18531;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region M315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
DR   PIR; JT0509; HVMS31.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION M315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13095 MW;  4562E03E53DC9E10 CRC64;

  Query Match             56.1%;  Score 341.5;  DB 1;  Length 116;
  Best Local Similarity   67.0%;  Pred. No. 1.2e-29;
  Matches   63;  Conservative   16;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|:|||:|:|:| || | ||||:|||| ||  |||:||| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYISYDGSNNYNPSL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR 95
              |:||::: |||:|:| |:|||||  ||| |||||
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116


RESULT 8
HV62_MOUSE
ID   HV62_MOUSE     STANDARD;      PRT;   117 AA.
AC   P18533;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 733 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; JT0510; HVMS73.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    117       IG HEAVY CHAIN V REGION 733.
FT   DOMAIN       19   >117       IG-LIKE.
FT   DISULFID     40    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13223 MW;  1595517827F976BE CRC64;

  Query Match             54.8%;  Score 334;  DB 1;  Length 117;
  Best Local Similarity   64.9%;  Pred. No. 7.5e-29;
  Matches   61;  Conservative   14;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|:::|:| |:| || :| | |||||| ||  ||||||||:|  | ||||
Db         24 ESGPGLVKPSQSIALTCTVTGISITTGNYRWSWIRQFPGNKLEWIGYIYYSAITSYNPSP 83

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR 95
              |||  :: |||:|:| | :||:|| ||| |||||
Db         84 KSRTTITRDTSKNQFFLEMNSLTAEDTATYYCAR 117


RESULT 9
HV43_MOUSE
```

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ID   HV43_MOUSE     STANDARD;      PRT;   144 AA.
AC   P01819;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOPC 141 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC       DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00768; CAA24149.1; -.
DR   PIR; A02094; G2MS14.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    144       IG HEAVY CHAIN V REGION MOPC 141.
FT   DOMAIN       20    130       IG-LIKE.
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15759 MW;  8E47A7CB3706D30A CRC64;

  Query Match             52.8%;  Score 321.5;  DB 1;  Length 144;
  Best Local Similarity   54.1%;  Pred. No. 2.1e-27;
  Matches   66;  Conservative   21;  Mismatches   24;  Indels   11;  Gaps    3;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||| |:|:||::| ||| |:   ||  :|:|| |||||||:| |: :|:| || :|
Db         25 ESGPGLVAPSQSLSITCTVSGFSLT--GYGVNWVRQPPGKGLEWLGTIWGNGSTDYNSTL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA--------RLDGY-TLDIWGQGTLVTV 112
              |||: :: | |:::  |::||:   ||| ||||        | | | ||| ||||| |||
Db         83 KSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSIYYYGRSDKYFTLDYWGQGTSVTV 142

Qy        113 SS 114
              ||
Db        143 SS 144


RESULT 10
HV02_XENLA
ID   HV02_XENLA     STANDARD;      PRT;   135 AA.
AC   P20957;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region XIG14 precursor (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03632; AAA49791.1; -.
DR   PIR; B31933; B31933.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN        19    135       IG HEAVY CHAIN V REGION XIG14.
FT   DOMAIN       20    128       IG-LIKE.
FT   NON_TER     135    135
SQ   SEQUENCE   135 AA;  15080 MW;  EBC467105C00732E CRC64;

  Query Match             49.9%;  Score 304;  DB 1;  Length 135;
  Best Local Similarity   51.3%;  Pred. No. 1.4e-25;
  Matches   59;  Conservative   19;  Mismatches   33;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||| |||:::| |:| |||  : |  |:  |||| |||||||||| |   |:|    ||
Db         23 ESGPGTVKPSESLRLTCTVSGFELSS--YHMHWIRQPPGKGLEWIGVIATGGSTAIADSL 80

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDGYTLDIWGQGTLVTVSS 114
              |:|: :: |  : :  |::| :   |||:|||||    ||  | |||||:|||:|
Db         81 KNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCAREYASGYNFDYWGQGTMVTVTS 135


RESULT 11
HV2B_HUMAN
ID   HV2B_HUMAN     STANDARD;      PRT;   120 AA.
AC   P01815;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region COR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02089; G1HUCO.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
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DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    110       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     94
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .).
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13226 MW;  158A8B29AE7EEB98 CRC64;

  Query Match             49.3%;  Score 300;  DB 1;  Length 120;
  Best Local Similarity   52.9%;  Pred. No. 3.4e-25;
  Matches   63;  Conservative   16;  Mismatches   30;  Indels   10;  Gaps    3;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| |||| |||:|:|  || |: | |    |||| |||||||:  |    : ||| ||
Db          6 ESGPALVKPTQTLTLTCTFSGFSLSSTGMCVGWIRQPPGKGLEWLARIDWDDDKYYNTSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD------GYTLDIWGQGTLVTVSS 114
              ::|: :| ||| |:  | :: |   ||| |||||:       || :|:||:|| |||||
Db         66 ETRLTISKDTSRNQVVLTMDPV---DTATYYCARITVIPAPAGY-MDVWGRGTPVTVSS 120


RESULT 12
HV40_MOUSE
ID   HV40_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01810;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig heavy chain V region J539.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PRELIMINARY SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=88217852; PubMed=3449853;
RA   Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA   Davies D.R.;
RT   "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT   study at 2.6-A resolution.";
RL   Proteins 1:74-80(1986).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC       BINDS GALACTAN.
DR   PIR; A02080; AVMSJ5.
DR   PDB; 2FBJ; 15-OCT-90.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   NON_TER     119    119
FT   STRAND        3      7
FT   STRAND       10     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   TURN         62     67
FT   STRAND       68     72
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92    100
FT   TURN        101    103
FT   STRAND      104    108
FT   STRAND      112    116
SQ   SEQUENCE   119 AA;  13240 MW;  577B4F1DB675C1F1 CRC64;

  Query Match             48.4%;  Score 295;  DB 1;  Length 119;
  Best Local Similarity   53.4%;  Pred. No. 1.1e-24;
  Matches   62;  Conservative   16;  Mismatches   34;  Indels    4;  Gaps    3;

Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIY-HSGNTYYNP 59
              |||| |||:|  :| |||| ||        |: ||:|| |||||||||  |:  ||   | |
Db          5 LESGGGLVQPGGSLKLSCAASGFDFSK--YWMSWVRQAPGKGLEWIGEIHPDSGTINYTP 62

Qy         60 SLKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLD-IWGQGTLVTVSS 114
              ||| :  :| | ::|   |::: | : |||:||||||  |  :  ||||||||||:
Db         63 SLKDKFIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYNAYWGQGTLVTVSA 118


RESULT 13
HV3A_HUMAN
ID   HV3A_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01762;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN TRO).
RX   MEDLINE=76023781; PubMed=809331;
RA   Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
RA   Hilschmann N.;
RT   "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
RT   II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT   structure of the complete IgA-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02045; A1HUTR.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    108       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13472 MW;  2E21A11DA04D80F9 CRC64;

  Query Match             48.1%;  Score 293;  DB 1;  Length 122;
  Best Local Similarity   47.5%;  Pred. No. 1.9e-24;
  Matches   57;  Conservative   21;  Mismatches   34;  Indels    8;  Gaps    3;

Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNT-YYNP 59
              ::|| |||||  :| |||  || | |   :| ||||: |||||:|: ||  ||:| ||
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Db          5 VQSGGGLVKPGGSLRLSCVASGFSFRD--FYMSWIRZTPGKGLZWVSYIGGSGSTLYYAD 62

Qy         60 SLKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG-----YTLDIWGQGTLVTVSS 114
              |:| |  :| | ::    | ::|:   :|||||||  :      ::|: ||:| ||||||
Db         63 SVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBPBWSTFSLBYWGZGBLVTVSS 122


RESULT 14
HV38_MOUSE
ID   HV38_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01808;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region T601.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC       THAT BINDS GALACTAN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02078; AVMST6.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       IG-LIKE.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13169 MW;  BC38CC84E6EA00E8 CRC64;

  Query Match             47.3%;  Score 288;  DB 1;  Length 119;
  Best Local Similarity   52.6%;  Pred. No. 6.4e-24;
  Matches   61;  Conservative   15;  Mismatches   36;  Indels    4;  Gaps    3;

Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTY-YNP 59
              |||| |||:|  :| |||| ||       |: ||:|| |||||||||  |    :|  | |
Db          5 LESGGGLVQPGGSLKLSCAASGFDF--SRYWMSWVRQAPGKGLEWIGEINPDSSTINYTP 62

Qy         60 SLKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGY-TLDIWGQGTLVTVSS 114
              ||| :  :| | ::|    |::: | : |||:||||||  |    |:|| || |||||
Db         63 SLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGYFDVWGAGTTVTVSS 118


RESULT 15
HV2C_HUMAN
ID   HV2C_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01816;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region DAW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC       SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02091; G1HUDW.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    113       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13045 MW;  4E13E00214BAD789 CRC64;

  Query Match             46.9%;  Score 285.5;  DB 1;  Length 119;
  Best Local Similarity   50.9%;  Pred. No. 1.2e-23;
  Matches   58;  Conservative   18;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| ||:| |||:|:|  || |:       :|||| ||: |||: :   : : ||  ||
Db          6 ESGPALVRPTQTLTLTCTFSGFSLSGETMCVAWIRQPPGEALEWLAWDILNDDKYYGASL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG-YTLDIWGQGTLVTVSS 114
              ::|:|:| |||:|:  | :|:|   ||| |||||  |    | |||| ||||||
Db         66 ETRLAVSKDTSKNQVVLSMNTVGPGDTATYYCARSCGSQYFDYWGQGILVTVSS 119


Search completed: August  8, 2004, 12:14:31
Job time : 7.21818 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 31.2636 Seconds
(without alignments)
1150.508 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	473	77.7	478	4	Q7Z379	Q7z379 homo sapien
2	451	74.1	150	4	O95973	O95973 homo sapien
3	446.5	73.3	119	4	Q9UL73	Q9ul73 homo sapien
4	432	70.9	496	4	Q96KX8	Q96kx8 homo sapien
5	430.5	70.7	492	4	Q7Z374	Q7z374 homo sapien
6	430	70.6	613	4	Q96EY0	Q96ey0 homo sapien
7	409.5	67.2	588	4	Q8WUX4	Q8wux4 homo sapien
8	409.5	67.2	597	4	Q9BU10	Q9bu10 homo sapien
9	409.5	67.2	618	4	Q96AA6	Q96aa6 homo sapien
10	408	67.0	139	4	Q86SX2	Q86sx2 homo sapien
11	405.5	66.6	597	4	Q9BQB8	Q9bqb8 homo sapien
12	405	66.5	130	4	Q8IZD7	Q8izd7 homo sapien
13	388	63.7	473	4	Q8TC63	Q8tc63 homo sapien
14	377.5	62.0	479	11	Q99M22	Q99m22 mus musculu
15	374	61.4	116	4	Q7Z3Y6	Q7z3y6 homo sapien
16	362	59.4	122	4	Q9UL75	Q9ul75 homo sapien
17	326	53.5	118	11	Q811U5	Q811u5 mus musculu
18	323	53.0	121	11	Q99NG4	Q99ng4 mus musculu
19	316.5	52.0	121	4	Q9UL96	Q9ul96 homo sapien
20	315	51.7	482	11	Q91X92	Q91x92 mus musculu
21	312.5	51.3	118	4	Q9UL74	Q9ul74 homo sapien
22	300	49.3	613	4	Q8WUK1	Q8wuk1 homo sapien
23	295.5	48.5	113	4	Q9UL90	Q9ul90 homo sapien
24	295.5	48.5	116	4	Q9UL93	Q9ul93 homo sapien
25	295	48.4	118	4	Q9UL72	Q9ul72 homo sapien
26	293.5	48.2	597	4	Q96BB9	Q96bb9 homo sapien
27	292	47.9	118	4	Q9UL91	Q9ul91 homo sapien
28	290.5	47.7	493	4	Q8NCL6	Q8ncl6 homo sapien
29	284.5	46.7	121	4	Q9UL71	Q9ul71 homo sapien
30	284	46.6	484	11	Q8VEA0	Q8vea0 mus musculu
31	282.5	46.4	119	5	Q9GYZ2	Q9gyz2 schistosoma
32	282.5	46.4	481	11	Q91WT1	Q91wt1 mus musculu
33	282	46.3	145	11	Q924R1	Q924r1 mus musculu
34	281.5	46.2	499	4	Q8N5K4	Q8n5k4 homo sapien
35	281	46.1	122	4	Q9UL84	Q9ul84 homo sapien
36	281	46.1	573	4	Q8WU38	Q8wu38 homo sapien
37	280	46.0	469	11	Q8R3V9	Q8r3v9 mus musculu
38	279	45.8	145	11	Q924P7	Q924p7 mus musculu
39	278	45.6	147	4	Q9Y509	Q9y509 homo sapien
40	277	45.5	124	6	Q9N0W6	Q9n0w6 oryctolagus
41	277	45.5	298	11	Q9QYF0	Q9qyf0 mus musculu
42	277	45.5	494	4	Q96K68	Q96k68 homo sapien
43	276.5	45.4	117	11	Q9QXE9	Q9qxe9 mus musculu
44	276	45.3	112	4	Q9HCC1	Q9hcc1 homo sapien
45	276	45.3	124	6	Q9N0W4	Q9n0w4 oryctolagus

ALIGNMENTS

RESULT 1
Q7Z379
ID Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN DKFZP686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 77.7%; Score 473; DB 4; Length 478;
Best Local Similarity 75.7%; Pred. No. 6.2e-41;
Matches 87; Conservative 17; Mismatches 9; Indels 2; Gaps 1;

```
Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| ||||| || |:|||||| ||:||||:||||:||:|||||||
Db         24 ESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTYYNPSL 83

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGY--TLDIWGQGTLVTVSS 114
              :||:::|:|||:|:|||||||:||||||||:|||  |     |||||||:|||||
Db         84 ESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVGLGTAFDIWGQGTVVTVSS 138
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RESULT 2
O95973

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ID   O95973      PRELIMINARY;      PRT;   150 AA.
AC   O95973;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH4 heavy chain variable region precursor (Fragment).
GN   IGM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT   "Clonal proliferation of IgM secreting B cell in the synovium of
RT   Behcet's patient with arthritis.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF103795; AAC79084.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    >150      VH4 HEAVY CHAIN VARIABLE REGION.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16315 MW;  85664E04938AA7C9 CRC64;

  Query Match             74.1%;  Score 451;  DB 4;  Length 150;
  Best Local Similarity   74.3%;  Pred. No. 2.8e-39;
  Matches   84;  Conservative   12;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::|||||| |||||| |  ||| |||| | ||||||| :::||: ||||||
Db         25 ESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDYYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||||:|||||||||||||||     | || ||:|||||
Db         85 KSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTMVTVSS 137


RESULT 3
Q9UL73
ID   Q9UL73      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13219 MW;  1BDB86B6420EA0BE CRC64;

  Query Match             73.3%;  Score 446.5;  DB 4;  Length 119;
  Best Local Similarity   74.1%;  Pred. No. 6.2e-39;
  Matches   86;  Conservative   12;  Mismatches   13;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| ||||||||||||:||:| | |||
Db          6 ESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYTPSL 63

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG---YTLDIWGQGTLVTVSS 114
              |||: :||| |:|:|||:| |:||||||||:||||     | | ||||||||||||
Db         64 KSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNWGPYYFDYWGQGTLVTVSS 119


RESULT 4
Q96KX8
ID   Q96KX8      PRELIMINARY;      PRT;   496 AA.
AC   Q96KX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016369; AAH16369.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53391 MW;  D346929849040D69 CRC64;

  Query Match             70.9%;  Score 432;  DB 4;  Length 496;
  Best Local Similarity   69.2%;  Pred. No. 1.3e-36;
  Matches   83;  Conservative   13;  Mismatches   16;  Indels    8;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||| ::||||:| |||||| |  ||| |||| ||||||||   |:|| |||||||
Db         25 ESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITYYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYT-------LDIWGQGTLVTVSS 114
              |||: :|||||:|: ||:: ||||||||||:|||  ||:       :| ||||||||||
Db         85 KSRVTISVDTSKNQLSLKVRSVTAADTAVYFCAR-HGYSRSGRTGAIDYWGQGTLVTVSS 143


RESULT 5
Q7Z374
ID   Q7Z374      PRELIMINARY;      PRT;   492 AA.
AC   Q7Z374;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686C02218 (Fragment).
GN   DKFZP686C02218.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
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RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538077; CAD98001.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   492 AA;  53776 MW;  1E7A15760F0CA74B CRC64;

  Query Match             70.7%;  Score 430.5;  DB 4;  Length 492;
  Best Local Similarity   71.6%;  Pred. No. 1.8e-36;
  Matches   83;  Conservative   13;  Mismatches   17;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||: :  ||| |||| |||||||||| ||:: ||||:|||
Db         37 ESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTYYSPSL 96

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-LDG--YTLDIWGQGTLVTVSS 114
              |||: : ||||:| ||||| |||||||||||| | ::|     | ||||||||||
Db         97 KSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYGWFDPWGQGTLVTVSS 152


RESULT 6
Q96EY0
ID   Q96EY0      PRELIMINARY;      PRT;   613 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67273 MW;  31214203FB8421E7 CRC64;

  Query Match             70.6%;  Score 430;  DB 4;  Length 613;
  Best Local Similarity   74.4%;  Pred. No. 2.7e-36;
  Matches   87;  Conservative    9;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||  |||||||| || ||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA----RLDGYTLDIWGQGTLVTVSS 114
              |||: ||||||:|:|||:|:|||||||||||||     |    |  ||||||||||
Db         83 KSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCASQPWELPTVGLFYWGQGTLVTVSS 139


RESULT 7
Q8WUX4
ID   Q8WUX4      PRELIMINARY;      PRT;   588 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   588 AA;  64438 MW;  FC60DBAD82B39FD7 CRC64;

  Query Match             67.2%;  Score 409.5;  DB 4;  Length 588;
  Best Local Similarity   66.7%;  Pred. No. 3.5e-34;
  Matches   80;  Conservative   14;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:||::||||:| | |||    ||||||||| |||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCARL--------DG-YTLDIWGQGTLVTVSS 114
              |: :|||||: : ||:|:|| ||||||||||:        || | :|:|||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 8
Q9BU10
ID   Q9BU10      PRELIMINARY;      PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

  Query Match             67.2%;  Score 409.5;  DB 4;  Length 597;
  Best Local Similarity   66.7%;  Pred. No. 3.6e-34;
  Matches   80;  Conservative   14;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:||::||||:| | |||    ||||||||| |||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCARL--------DG-YTLDIWGQGTLVTVSS 114
              |: :|||||: : ||:|:|| ||||||||||:        || | :|:|||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 9
```

```
Q96AA6
ID   Q96AA6      PRELIMINARY;      PRT;   618 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   618 AA;  67758 MW;  96DBD4C7C696E0A6 CRC64;

  Query Match             67.2%;  Score 409.5;  DB 4;  Length 618;
  Best Local Similarity   66.7%;  Pred. No. 3.7e-34;
  Matches   80;  Conservative   14;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:||::||||:| | |||    ||||||||| ||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCARL--------DG-YTLDIWGQGTLVTVSS 114
              |: :|||||: : ||:|:|| ||||||||||:        || | :|:|||||  |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 10
Q86SX2
ID   Q86SX2      PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)
DE   of Homo sapiens (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Plasmid.
FT   NON_TER       1       1
SQ   SEQUENCE   139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;

  Query Match             67.0%;  Score 408;  DB 4;  Length 139;
  Best Local Similarity   80.9%;  Pred. No. 8.1e-35;
  Matches   76;  Conservative   11;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| |||||||||||:||:| |||||
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 95

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR 95
              |||: :|||||:|:|||:|:|||||||||||||
Db         96 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129


RESULT 11
Q9BQB8
ID   Q9BQB8      PRELIMINARY;      PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle, and Lymph;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;

  Query Match             66.6%;  Score 405.5;  DB 4;  Length 597;
  Best Local Similarity   66.7%;  Pred. No. 9.4e-34;
  Matches   80;  Conservative   13;  Mismatches   16;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:||::||||:| | |||    ||||||||| ||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGITNYNPSLKS 84

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCARL--------DG-YTLDIWGQGTLVTVSS 114
              |: :|||||: : ||:|:|| ||||||||||:        || | :|:|||||  |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 12
Q8IZD7
ID   Q8IZD7      PRELIMINARY;      PRT;   130 AA.
AC   Q8IZD7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-thyroglobulin heavy chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jang Y.-J., Chung J., Park J.-Y.;
RT   "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT   Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145445; AAN64329.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  13901 MW;  036131FC6EC1551E CRC64;

  Query Match             66.5%;  Score 405;  DB 4;  Length 130;
  Best Local Similarity   65.6%;  Pred. No. 1.5e-34;
  Matches   82;  Conservative   13;  Mismatches   18;  Indels   12;  Gaps    4;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNT-----Y 56
              :||||||||::||||:| |||||| |  ||| |||| |||||||||| :|:||:|     |
Db          6 QSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTYSGSPY 65

Qy         57 YNPSLKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDG---YT-LDIWGQGTL 109
              | |||:||: :|||||:|: ||||:||||||||||||      |   |     |||| |
Db         66 YAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFQHWGQGFL 125

Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130


RESULT 13
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   GO; GO:0005507; F:copper ion binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match             63.7%;  Score 388;  DB 4;  Length 473;
  Best Local Similarity   65.2%;  Pred. No. 4.7e-32;
  Matches   75;  Conservative   13;  Mismatches   23;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||:||: ||||:| ||| |: |  ||| |:|| |||||||| |  ||| ||:|||
Db         32 ESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQPPGKGLEWIGTINFSGNMYYSPSL 91

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR---LDGYTLDIWGQGTLVTVS 113
              :||: || | ||| | |:|:||||||||||||    : |:    |||| ||:||
Db         92 RSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAGHLVMGFGAH-WGQGKLVSVS 145


RESULT 14
Q99M22
ID   Q99M22      PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768E39A138918892 CRC64;

  Query Match             62.0%;  Score 377.5;  DB 11;  Length 479;
  Best Local Similarity   64.9%;  Pred. No. 6e-31;
  Matches   74;  Conservative   18;  Mismatches   19;  Indels    3;  Gaps    3;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|:|||:|:|:| || | ||||:|||| ||  |||:||| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYINYDGSNNYNPSL 82

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYT-LDIWGQGTLVTVSS 114
              |:||::: |||:|:| |:|||||  ||| ||||   ||:    ||||||||||:
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCAS-RGYSWFPNWGQGTLVTVSA 135


RESULT 15
Q7Z3Y6
ID   Q7Z3Y6      PRELIMINARY;      PRT;   116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   VH4-34.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RT   "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT   indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT   cell precursor in a germinal center.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
FT   NON_TER       1      1
```

```
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A846616C908 CRC64;

  Query Match             61.4%;  Score 374;  DB 4;  Length 116;
  Best Local Similarity   64.9%;  Pred. No. 2.3e-31;
  Matches   72;  Conservative   14;  Mismatches   13;  Indels   12;  Gaps    2;

Qy          4 GPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:||::|||||||| |||    ||||:|||| ||||||||| | |||:| |||||||
Db          8 GAGLLKPSETLSLSCAVYGGSF--SGYYWNWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 65

Qy         64 RIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD----------GYTLDIW 104
              |: :|||||:|: ||:|:|||||||||||||| :          | :|:|
Db         66 RVTISVDTSKNQLSLKLSSVTAADTAVYYCARGEIVVVPAASYYYYYMDVW 116


Search completed: August  8, 2004, 12:17:44
Job time : 32.2636 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	100.0	114	5	ABG30445	Abg30445 Human IgE
2	547	89.8	114	5	ABG30447	Abg30447 Human IgE
3	546	89.7	114	5	ABG30446	Abg30446 Human IgE
4	506.5	83.2	123	2	AAW78433	Aaw78433 Antibody
5	506.5	83.2	123	5	ABB97976	Abb97976 Heavy cha
6	505	82.9	252	5	ABP45983	Abp45983 Human BLy
7	502	82.4	123	4	AAB62745	Aab62745 Human HIV
8	501.5	82.3	117	7	ADC99784	Adc99784 Anti-huma
9	501.5	82.3	117	7	ADD05388	Add05388 Anti-MUC1
10	500.5	82.2	251	6	ABJ19829	Abj19829 Human VEG
11	499.5	82.0	120	4	AAB62775	Aab62775 Human HIV
12	499	81.9	473	4	AAB36206	Aab36206 Human imm
13	498.5	81.9	253	5	ABP45608	Abp45608 Human BLy
14	496	81.4	172	3	AAY93713	Aay93713 The heavy
15	496	81.4	172	6	AAE35892	Aae35892 Human 2.1
16	495.5	81.4	122	4	AAB62765	Aab62765 Human HIV
17	494.5	81.2	119	7	ADC99796	Adc99796 Anti-huma
18	494.5	81.2	119	7	ADD05400	Add05400 Anti-MUC1
19	493.5	81.0	129	5	AAU81275	Aau81275 Human trk
20	490	80.5	126	3	AAB30584	Aab30584 A human v
21	490	80.5	126	5	ABP54970	Abp54970 Anti-idio
22	490	80.5	130	5	AAU81273	Aau81273 Human trk
23	490	80.5	251	5	ABG80712	Abg80712 Amyloid p
24	490	80.5	254	5	ABG80713	Abg80713 Amyloid p
25	490	80.5	263	5	ABG80714	Abg80714 Human IgG
26	489.5	80.4	117	7	ADC99776	Adc99776 Anti-huma
27	489.5	80.4	117	7	ADD05380	Add05380 Anti-MUC1
28	489	80.3	118	2	AAY06385	Aay06385 Humanised
29	483.5	79.4	129	5	AAU81276	Aau81276 Human trk
30	482	79.1	256	5	ABP45596	Abp45596 Human BLy
31	482	79.1	487	4	AAB90607	Aab90607 Human sec
32	482	79.1	487	5	ABG65445	Abg65445 Human alb
33	481	79.0	246	3	AAY15126	Aay15126 Anti-muri
34	479	78.7	118	2	AAY06386	Aay06386 Humanised
35	477	78.3	118	2	AAY06383	Aay06383 Humanised
36	476.5	78.2	117	7	ADC99804	Adc99804 Anti-huma
37	476.5	78.2	117	7	ADD05408	Add05408 Anti-MUC1
38	474	77.8	252	5	ABP45318	Abp45318 Human BLy
39	474	77.8	256	5	ABP45734	Abp45734 Human BLy
40	473	77.7	229	3	AAB30593	Aab30593 Variable
41	472.5	77.6	121	7	ADC99808	Adc99808 Anti-huma
42	472.5	77.6	121	7	ADD05412	Add05412 Anti-MUC1
43	471.5	77.4	119	2	AAR30143	Aar30143 MAb GAH v
44	471.5	77.4	119	2	AAW27554	Aaw27554 Human Ab
45	471.5	77.4	119	6	ABP98691	Abp98691 Human GAH

ALIGNMENTS

RESULT 1
ABG30445
ID ABG30445 standard; protein; 114 AA.
XX
AC ABG30445;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 94 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89637.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 36; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 609; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
```

RESULT 2
ABG30447
ID ABG30447 standard; protein; 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89639.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 38; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 100 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 89.8%; Score 547; DB 5; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.1e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||:|||||:| |||||||||||||||||| |||||||| ||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||: |||||||:| |||||:|||||||||||||| |||||| ||||||||||
Db         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 3
ABG30446
ID ABG30446 standard; protein; 114 AA.
XX
AC ABG30446;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"

FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89638.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 37; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 89.7%; Score 546; DB 5; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.4e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              |||||||||:|||||:| |||||||||||||:|| |||||||| ||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||| |||||||:| ||||| |||||||||||||| |||||| ||||||||||
Db         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 4
AAW78433
ID AAW78433 standard; protein; 123 AA.
XX
AC AAW78433;
XX
DT 11-MAY-1999 (first entry)
XX
DE Antibody heavy chain targeted to obr clone 26.
XX
KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
XX
OS Synthetic.
XX
PN WO9850431-A2.
XX
PD 12-NOV-1998.
XX
PF 30-APR-1998; 98WO-US008762.
XX
PR 02-MAY-1997; 97US-00850058.
PR 24-JUN-1997; 97US-0050661P.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon R, Carter PJ, Merchant AM, Presta LG;
XX
DR WPI; 1999-070091/06.
XX
PT Selective preparation of multispecific antibodies - with heteromultimeric
PT heavy chain and common light chain components, useful for, e.g. in vivo
PT diagnosis of cancer.
XX
PS Example 4; Fig 5; 69pp; English.
XX
CC This sequence represents the heavy chain variable region for an antibody
CC that binds to the obr clone 26 protein. The sequence encoding the chain
CC is generated by a new method for preparing a multispecific Ab comprising
CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP
CC comprises a multimerisation domain (MD) forming an interface positioned
CC to interact with an interface of a MD of the extra PP; and (ii) the first
CC and extra PPs each have a binding domain, which comprises a heavy chain
CC and a light chain, where the variable light chains of the first and extra
CC PPs comprise a common sequence. The method comprises: (a) culturing a
CC host cell comprising nucleic acid encoding the first PP and extra PP, and
CC the variable light chain, such that the nucleic acid is expressed; and
CC (b) recovering the multispecific Ab from the culture. The method prepares
CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins
CC and Ab-immunoadhesin chimeras. The method allows for the enhanced
CC formation of the desired heteromultimer relative to the undesired
CC heteromultimers and homomultimers. The Abs can be used in immunoassays
CC and for the in vitro or in vivo diagnosis of various diseases, such as
CC cancer
XX
SQ Sequence 123 AA;

Query Match 83.2%; Score 506.5; DB 2; Length 123;
Best Local Similarity 79.0%; Pred. No. 6.5e-39;
Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              :|||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD-----GYTLDIWGQGTLVTVSS 114
              ||||: :|||||:|:|||:|:|||||||||||||:|         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 5
ABB97976
ID ABB97976 standard; protein; 123 AA.
XX
AC ABB97976;
XX
DT 06-SEP-2002 (first entry)
XX
DE Heavy chain variable region from antibody obr.26.
XX
KW Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
KW antiviral; vaccine; tumour.
XX
OS Synthetic.
XX
PN US2002062010-A1.
XX
PD 23-MAY-2002.

XX
PF 23-MAY-2001; 2001US-00863693.
XX
PR 02-MAY-1997; 97US-0046816P.
PR 30-APR-1998; 98US-00070166.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon WR, Carter PJ, Merchant AM, Presta LG;
XX
DR WPI; 2002-499676/53.
XX
PT New multispecific antibodies having heteromultimeric and common
PT components are useful to direct treatment to a target site such as a
PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
PT treat infectious disease.
XX
PS Example 4; Fig 5; 36pp; English.
XX
CC The invention relates to a new multispecific antibody, comprising at
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1
CC has a multimerisation domain forming an interface positioned to interact
CC with an interface of a multimerisation domain of PP2, and both
CC polypeptides each comprise a binding domain consisting a heavy chain and
CC a variable light chain, where the light chain has a sequence common to
CC both polypeptides. Hetromultimers of the inventions include bispecific
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin
CC chimeras. The activity of antibodies of the invention may be described
CC as, cytostatic, antibacterial and antiviral. The heteromultimer can be
CC used for redirected cytotoxicity, for example to kill tumour cells, as a
CC vaccine adjuvant, for delivering thrombolytic agents to clots, for
CC converting enzyme activated prodrugs at a target site such as a tumour,
CC for treating infectious diseases, for targeting immune complexes to cell
CC surface receptors or for delivering immunotoxins to tumour cells. The
CC current sequence represents the heavy chain variable region from antibody
CC obr.26 used in the construction of bispecific antibodies
XX
SQ Sequence 123 AA;

Query Match 83.2%; Score 506.5; DB 5; Length 123;
Best Local Similarity 79.0%; Pred. No. 6.5e-39;
Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              :|||||||||:|||||:| |||||| ||||||||||||||||||||||:||:||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD-----GYTLDIWGQGTLVTVSS 114
              ||||: :|||||:|:|||:|:|||||||||||||:|         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 6
ABP45983
ID ABP45983 standard; protein; 252 AA.
XX
AC ABP45983;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1994.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2779-2780; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;

Query Match 82.9%; Score 505; DB 5; Length 252;
Best Local Similarity 78.2%; Pred. No. 1.9e-38;
Matches 93; Conservative 12; Mismatches 8; Indels 6; Gaps 1;

```
Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| || ||||||||||:||||||||||||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQHPGEGLEWIGYIYHSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL------DGYTLDIWGQGTLVTVSS 114
              |||::||||||:|::||:|:|||||||||||||||        | | |||||:|||||
Db         66 KSRVSMSVDTSKNQYSLKLSSVTAADTAVYYCARLRPDADYGDYGFDYWGQGTMVTVSS 124
```

RESULT 7
AAB62745
ID AAB62745 standard; protein; 123 AA.
XX
AC AAB62745;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.

```
XX
PF   23-JUN-2000; 2000WO-US017327.
XX
PR   30-JUN-1999;   99US-0141701P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   N-PSDB; AAF29046.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal.
XX
PS   Claim 1; Page 50; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ   Sequence 123 AA;

  Query Match             82.4%;  Score 502;  DB 4;  Length 123;
  Best Local Similarity   79.5%;  Pred. No. 1.7e-38;
  Matches   93;  Conservative   11;  Mismatches    9;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          7 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYNSGSTYYNPSL 66

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL----DGYTLDIWGQGTLVTVSS 114
              |||: :|:|||:|||||:|:|||||||||||||        : | ||||||||||
Db         67 KSRVTISIDTSKNKFSLKLSSVTAADTAVYYCARAAYCGGDCSFDYWGQGTLVTVSS 123


RESULT 8
ADC99784
ID   ADC99784 standard; protein; 117 AA.
XX
AC   ADC99784;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.
XX
KW   anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW   cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW   cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW   lung cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO2003057838-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041581.
XX
PR   28-DEC-2001; 2001US-0346299P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Gudas J;
XX
DR   WPI; 2003-587113/55.
DR   N-PSDB; ADC99786.
XX
PT   New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT   or condition associated with expression of MUC18 in a patient, e.g.
PT   tumors, cancers, and other malignancies.
XX
PS   Claim 1; SEQ ID NO 13; 78pp; English.
XX
CC   The invention relates to a novel isolated monoclonal antibody comprising
CC   a heavy or light chain amino acid or a heavy or light chain variable
CC   domain where the antibody binds to MUC18. The monoclonal antibody of the
CC   invention demonstrates cytostatic activity and may be useful for treating
CC   a disease or condition associated with the expression of MUC18 on the
CC   cell surface such as tumours, specifically melanoma, oesophageal,
CC   pancreatic or colorectal tumours, carcinomas, particularly cervical
CC   carcinomas and cervical intraepithelial neoplasia and cancers including
CC   colorectal, breast or lung cancer, as well as other malignancies. The
CC   current sequence is that of the anti-human MUC18 monoclonal antibody
CC   heavy chain protein of the invention.
XX
SQ   Sequence 117 AA;

  Query Match             82.3%;  Score 501.5;  DB 7;  Length 117;
  Best Local Similarity   81.4%;  Pred. No. 1.8e-38;
  Matches   92;  Conservative   13;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||:|||||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| :|   | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-EGDGFDYWGQGTLVTVSS 117


RESULT 9
ADD05388
ID   ADD05388 standard; protein; 117 AA.
XX
AC   ADD05388;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
XX
KW   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW   antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2003057006-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041582.
XX
PR   28-DEC-2001; 2001US-0346460P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Gudas J,  Bar-Eli M;
XX
DR   WPI; 2003-577496/54.
DR   N-PSDB; ADD05390.
XX
PT   Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT   treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT   associated with melanoma, or increasing survival of an animal having a
PT   metastatic tumor.
XX
PS   Claim 1; SEQ ID NO 13; 87pp; English.
XX
CC   The invention relates to a novel monoclonal antibody used for inhibiting
CC   tumour growth in an animal. The tumour inhibition process comprises
CC   selecting an animal in need of treatment for a tumour, providing a
CC   monoclonal antibody comprising a heavy chain amino acid, where the
CC   antibody consists of any one of 10 fully defined sequences of 117-123
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```
CC   amino acids given in the specification, and where the monoclonal antibody
CC   binds MUC18, and contacting the tumour with the antibody resulting in
CC   inhibited proliferation of the cells. The monoclonal antibody has
CC   cytostatic and can be used in the production of a vaccine. The monoclonal
CC   antibodies against the MUC18 antigen are useful for diagnosing and
CC   treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC   tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC   increasing survival of an animal having a metastatic tumour. This
CC   sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC   protein of the invention.
XX
SQ   Sequence 117 AA;

  Query Match             82.3%;  Score 501.5;  DB 7;  Length 117;
  Best Local Similarity   81.4%;  Pred. No. 1.8e-38;
  Matches   92;  Conservative   13;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||:|||||||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| :|    | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-EGDGFDYWGQGTLVTVSS 117


RESULT 10
ABJ19829
ID   ABJ19829 standard; protein; 251 AA.
XX
AC   ABJ19829;
XX
DT   10-APR-2003  (first entry)
XX
DE   Human VEGF-2 related protein SEQ ID No 75.
XX
KW   Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic;
KW   antiarthritic; antidiabetic; ophthalmological; antiallergic;
KW   immunosuppressive; dermatological; antipsoriatic; vulnerary; antibody;
KW   CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;
KW   proliferative disorder; cardiovascular disorder; arrhythmia;
KW   cerebrovascular disorder; cerebral anoxia; inflammatory disease;
KW   infectious disease; autoimmune disease; rheumatoid arthritis;
KW   Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;
KW   angiogenesis; wound healing; vascular tissue repair; human.
XX
OS   Homo sapiens.
XX
PN   WO200283704-A1.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US011474.
XX
PR   13-APR-2001; 2001US-0283385P.
PR   24-JAN-2002; 2002US-0350366P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Albert VR,  Ruben SM,  Wager RE;
XX
DR   WPI; 2003-092991/08.
XX
PT   New isolated polynucleotide encoding an antibody which inhibits a VEGF-2
PT   polypeptide, useful for diagnosing, treating or preventing diseases
PT   associated with aberrant VEGF-2 expression or function, e.g. cancer or
PT   inflammation.
XX
PS   Disclosure; Page 385-386; 425pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a first
CC   antibody at least 95-100% identical to a second antibody comprising an
CC   amino acid sequence selected from at least one, two or three CDR
CC   region(s) of a VH or VL domain where the first antibody
CC   immunospecifically inhibits a VEGF-2 polypeptide. The isolated
CC   polynucleotide is useful in diagnosing, treating, preventing, prognosing,
CC   ameliorating or monitoring diseases associated with aberrant VEGF-2 or
CC   VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,
CC   such as cancer and other proliferative disorders, cardiovascular
CC   disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral
CC   anoxia), inflammatory diseases, infectious diseases, autoimmune diseases
CC   (e.g. rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),
CC   diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and
CC   antibodies may also be used to stimulate angiogenesis, wound healing, and
CC   promoting vascular tissue repair. The polynucleotide and polypeptide may
CC   also be used for in vitro purposes related to scientific research,
CC   synthesis of DNA and manufacture of DNA vectors, and for the production
CC   of diagnostics and therapeutics to treat human diseases. This sequence
CC   represents a human VEGF-2 related protein of the invention
XX
SQ   Sequence 251 AA;

  Query Match             82.2%;  Score 500.5;  DB 6;  Length 251;
  Best Local Similarity   79.7%;  Pred. No. 5e-38;
  Matches   94;  Conservative   13;  Mismatches    6;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:|:|||||| | |||||||||||||||||||||:|||||||||
Db          6 ESGPGLVKPSQTLSLTCSVSGGSISSRGYYWSWIRQHPGKGLEWIGYIYHNGNTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR---LDGYT--LDIWGQGTLVTVSS 114
              |||| ||||||:|:|||:|:||||||||||:|||   : | :   |:||:|||||||
Db         66 KSRITMSVDTSKNQFSLKLSSVTAADTAVYFCARDKVVTGISGGFDLWGRGTLVTVSS 123


RESULT 11
AAB62775
ID   AAB62775 standard; protein; 120 AA.
XX
AC   AAB62775;
XX
DT   03-APR-2001  (first entry)
XX
DE   Human HIV-1 monoclonal antibody SEQ ID NO: 74.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200100678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US017327.
XX
PR   30-JUN-1999;   99US-0141701P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   N-PSDB; AAF29076.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal.
XX
PS   Claim 1; Page 69; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection
```

```
XX
SQ   Sequence 120 AA;

  Query Match            82.0%;  Score 499.5;  DB 4;  Length 120;
  Best Local Similarity  81.0%;  Pred. No. 2.8e-38;
  Matches   94;  Conservative   12;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||||:||:|||||||
Db          7 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 66

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR---LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||   :| :  | ||||||||||
Db         67 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVVVDWF--DPWGQGTLVTVSS 120


RESULT 12
AAB36206
ID   AAB36206 standard; protein; 473 AA.
XX
AC   AAB36206;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human immune system associated protein HISAP-4.
XX
KW   Human; immune system associated protein; HISAP-4; immune disorder;
KW   infection; autoimmune disease; cancer.
XX
OS   Homo sapiens.
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;   98US-00049672.
XX
PR   27-MAR-1998;   98US-00049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT,  Yue H,  Lal P,  Corley NC,  Guegler KJ,  Baughn MR;
PI   Hillman JL,  Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   N-PSDB; AAC66522.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing immune
PT   or cell proliferative disorders or infections.
XX
PS   Claim 1; Col 53-56; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ   Sequence 473 AA;

  Query Match            81.9%;  Score 499;  DB 4;  Length 473;
  Best Local Similarity  78.2%;  Pred. No. 1.3e-37;
  Matches   93;  Conservative   13;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:|||||||| |||||||||| |||||||||||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD------GYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| |      | :| ||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143


RESULT 13
ABP45608
ID   ABP45608 standard; protein; 253 AA.
XX
AC   ABP45608;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1619.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 2335-2336; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 253 AA;

  Query Match            81.9%;  Score 498.5;  DB 5;  Length 253;
  Best Local Similarity  77.9%;  Pred. No. 7.6e-38;
  Matches   95;  Conservative   12;  Mismatches    6;  Indels    9;  Gaps    3;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||:||:|||||||
```

```
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDG--YT--LDIWGQGTLVTV 112
              |||: :|:|||:|:|||:|:||||||||||||| |     | |  ||   |||||:||||||
Db         66 KSRVTISIDTSKNQFSLKLSSVTAADTAVYYCVRSYYDILTGRPYTDAFDIWGKGTLVTV 125

Qy        113 SS 114
              ||
Db        126 SS 127
```

RESULT 14
AAY93713
ID AAY93713 standard; protein; 172 AA.
XX
AC AAY93713;
XX
DT 03-OCT-2000 (first entry)
XX
DE The heavy chain of immunoglobulin clone 2.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.
XX
OS Homo sapiens.
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR WPI; 2000-442647/38.
DR N-PSDB; AAA46876.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
PS Claim 2; Fig 1G; 157pp; English.
XX
CC The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 172 AA;

```
  Query Match             81.4%;  Score 496;  DB 3;  Length 172;
  Best Local Similarity   79.8%;  Pred. No. 8.6e-38;
  Matches   91;  Conservative   12;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLK 62
              |||||||:| |||:| |||||| |||:||||||||||||||||||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YTLDIWGQGTLVTVSS 114
```

```
              ||: :|||||:|:|||:|:||||||||||||||  |  | :|:||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114
```

RESULT 15
AAE35892
ID AAE35892 standard; protein; 172 AA.
XX
AC AAE35892;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human 2.1.3 anti-CTLA-4 antibody heavy chain.
XX
KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW cancer.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Region   24. .31
FT   /note= "Complementarity determining region (CDR) 1"
FT Region   45. .61
FT   /note= "Complementarity determining region (CDR) 2"
FT Region   94. .103
FT   /note= "Complementarity determining region (CDR) 3"
XX
PN EP1262193-A1.
XX
PD 04-DEC-2002.
XX
PF 23-MAY-2002; 2002EP-00253652.
XX
PR 23-MAY-2001; 2001US-0293042P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Hanson DC, Mueller EE;
XX
DR WPI; 2003-131215/13.
XX
PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
PT preparation of medicament for the treatment of cancer.
XX
PS Disclosure; Fig 3; 76pp; English.
XX
CC The invention relates to the use of human anti-cytotoxic T lymphocyte
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC cancer, cancer of the anal region, stomach cancer, breast cancer,
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC The present sequence is human anti-CTLA-4 antibody heavy chain
XX
SQ Sequence 172 AA;

```
  Query Match             81.4%;  Score 496;  DB 6;  Length 172;
  Best Local Similarity   79.8%;  Pred. No. 8.6e-38;
  Matches   91;  Conservative   12;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLK 62
              |||||||:| |||:| |||||| |||:||||||||||||||||||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YTLDIWGQGTLVTVSS 114
              ||: :|||||:|:|||:|:||||||||||||||  |  | :|:||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114
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Job time : 48.8091 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 38.5182 Seconds
(without alignments)
928.389 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	100.0	114	14	US-10-027-725A-7	Sequence 7, Appli
2	556	91.3	114	14	US-10-027-725A-9	Sequence 9, Appli
3	546	89.7	114	14	US-10-027-725A-8	Sequence 8, Appli
4	519	85.2	122	15	US-10-309-762-147	Sequence 147, App
5	518.5	85.1	121	15	US-10-309-762-152	Sequence 152, App
6	517.5	85.0	125	15	US-10-309-762-11	Sequence 11, Appl
7	514.5	84.5	121	15	US-10-309-762-151	Sequence 151, App
8	512	84.1	118	15	US-10-309-762-138	Sequence 138, App
9	512	84.1	120	15	US-10-309-762-13	Sequence 13, Appl
10	512	84.1	120	15	US-10-309-762-144	Sequence 144, App
11	509.5	83.7	123	15	US-10-309-762-12	Sequence 12, Appl
12	508.5	83.5	123	15	US-10-309-762-10	Sequence 10, Appl
13	508.5	83.5	123	15	US-10-309-762-18	Sequence 18, Appl
14	508.5	83.5	123	15	US-10-309-762-19	Sequence 19, Appl
15	508.5	83.5	125	15	US-10-309-762-8	Sequence 8, Appli
16	508.5	83.5	125	15	US-10-309-762-16	Sequence 16, Appl
17	506.5	83.2	119	15	US-10-309-762-131	Sequence 131, App
18	505.5	83.0	119	15	US-10-309-762-140	Sequence 140, App
19	505	82.9	252	10	US-09-880-748-1994	Sequence 1994, Ap
20	505	82.9	252	12	US-10-293-418-1994	Sequence 1994, Ap
21	504.5	82.8	125	15	US-10-309-762-153	Sequence 153, App
22	504	82.8	120	15	US-10-309-762-139	Sequence 139, App
23	503.5	82.7	127	15	US-10-309-762-14	Sequence 14, Appl
24	503	82.6	124	15	US-10-309-762-75	Sequence 75, Appl
25	503	82.6	143	15	US-10-309-762-96	Sequence 96, Appl
26	501.5	82.3	117	14	US-10-330-613-13	Sequence 13, Appl
27	501.5	82.3	117	14	US-10-330-530-13	Sequence 13, Appl
28	501.5	82.3	117	16	US-10-660-357-13	Sequence 13, Appl
29	500.5	82.2	251	14	US-10-120-414-75	Sequence 75, Appl
30	498.5	81.9	253	10	US-09-880-748-1619	Sequence 1619, Ap
31	498.5	81.9	253	12	US-10-293-418-1619	Sequence 1619, Ap
32	497	81.6	110	15	US-10-309-762-74	Sequence 74, Appl
33	497	81.6	121	12	US-10-453-698-137	Sequence 137, App
34	497	81.6	121	15	US-10-308-817-137	Sequence 137, App
35	496.5	81.5	123	15	US-10-309-762-17	Sequence 17, Appl
36	496	81.4	172	14	US-10-153-382-21	Sequence 21, Appl
37	495.5	81.4	123	15	US-10-309-762-9	Sequence 9, Appli
38	494.5	81.2	119	14	US-10-330-613-25	Sequence 25, Appl
39	494.5	81.2	119	14	US-10-330-530-25	Sequence 25, Appl
40	494.5	81.2	119	16	US-10-660-357-25	Sequence 25, Appl
41	493.5	81.0	129	16	US-10-312-316-47	Sequence 47, Appl
42	493	81.0	221	10	US-09-972-656-80	Sequence 80, Appl
43	490	80.5	126	9	US-09-974-449-6	Sequence 6, Appli
44	490	80.5	130	16	US-10-312-316-45	Sequence 45, Appl
45	489.5	80.4	117	14	US-10-330-613-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match 100.0%; Score 609; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
```

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:

```
;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-9

  Query Match            91.3%;  Score 556;  DB 14;  Length 114;
  Best Local Similarity   90.4%;  Pred. No. 3.1e-45;
  Matches  103;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||:|||||:| ||||||||||||||||| ||||||||||||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||: ||||||:| |||||:|||||||||||||| |||||| ||||||||||
Db         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114


RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-8

  Query Match            89.7%;  Score 546;  DB 14;  Length 114;
  Best Local Similarity   89.5%;  Pred. No. 2.8e-44;
  Matches  102;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||:|||||:| ||||||||||||||:|| |||||||| ||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              ||||| ||||||:| ||||| |||||||||||||| |||||| ||||||||||
Db         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114


RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-147

  Query Match            85.2%;  Score 519;  DB 15;  Length 122;
  Best Local Similarity   81.2%;  Pred. No. 1.1e-41;
  Matches   95;  Conservative   12;  Mismatches    6;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR----LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||     | || :|:||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYDILTGYGMDVWGQGTTVTVSS 122


RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-152

  Query Match            85.1%;  Score 518.5;  DB 15;  Length 121;
  Best Local Similarity   81.9%;  Pred. No. 1.2e-41;
  Matches   95;  Conservative   11;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD---GYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||  |   ||  |||||||:|||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAYYDILTGYAFDIWGQGTMVTVSS 121


RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
```

```
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-11

  Query Match             85.0%;  Score 517.5;  DB 15;  Length 125;
  Best Local Similarity   81.7%;  Pred. No. 1.6e-41;
  Matches   98;  Conservative    9;  Mismatches    6;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||:||||||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGNTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDGY--TLDIWGQGTLVTVSS 114
              |||| :|||||:|:|||:|:|||||||||||||     | ||    |||||||:|||||
Db         66 KSRITISVDTSKNQFSLKLSSVTAADTAVYYCARTYYDFLTGYPDAFDIWGQGTMVTVSS 125


RESULT 7
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-151

  Query Match             84.5%;  Score 514.5;  DB 15;  Length 121;
  Best Local Similarity   81.0%;  Pred. No. 2.9e-41;
  Matches   94;  Conservative   13;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL---DGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||:    || :|:|||||  |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVLLWFGYGMDVWGQGTTVTVSS 121


RESULT 8
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-138

  Query Match             84.1%;  Score 512;  DB 15;  Length 118;
  Best Local Similarity   83.2%;  Pred. No. 4.9e-41;
  Matches   94;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||  |   | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYGSGSDYWGQGTLVTVSS 118


RESULT 9
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-13

  Query Match             84.1%;  Score 512;  DB 15;  Length 120;
  Best Local Similarity   81.9%;  Pred. No. 5e-41;
  Matches   95;  Conservative   12;  Mismatches    5;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| |||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYT---LDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| |||      |:||:||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 10
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
```

```
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-144

  Query Match            84.1%;  Score 512;  DB 15;  Length 120;
  Best Local Similarity  81.9%;  Pred. No. 5e-41;
  Matches   95;  Conservative   12;  Mismatches    5;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYT---LDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||| |||     |:||:|||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 11
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-12

  Query Match            83.7%;  Score 509.5;  DB 15;  Length 123;
  Best Local Similarity  78.8%;  Pred. No. 8.8e-41;
  Matches   93;  Conservative   13;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:|| |||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGTTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL-----DGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||:     : | :|:||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVLLWFGEDYGVDVWGQGTTVTVSS 123


RESULT 12
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-10

  Query Match            83.5%;  Score 508.5;  DB 15;  Length 123;
  Best Local Similarity  80.5%;  Pred. No. 1.1e-40;
  Matches   95;  Conservative   10;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARL-----DGYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||:     | || ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARAGKYYGSGSYLDYWGQGTLVTVSS 123


RESULT 13
US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-18

  Query Match            83.5%;  Score 508.5;  DB 15;  Length 123;
  Best Local Similarity  80.5%;  Pred. No. 1.1e-40;
  Matches   95;  Conservative   10;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSINSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||||:|||:|:|||||||||||||        | ||:||||| |||||
Db         66 KSRVIISVDTSENQFSLKLSSVTAADTAVYYCARERVTDYYYYGLDVWGQGTTVTVSS 123


RESULT 14
US-10-309-762-19
; Sequence 19, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
```

```
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-19

  Query Match             83.5%;  Score 508.5;  DB 15;  Length 123;
  Best Local Similarity   80.5%;  Pred. No. 1.1e-40;
  Matches   95;  Conservative   10;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| ||||||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSINSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDGYTLDIWGQGTLVTVSS 114
              |||: :|||||||:|||:|:|||||||||||||        | ||:||||| |||||
Db         66 KSRVIISVDTSENQFSLKLSSVTAADTAVYYCARERVTDYYYYGLDVWGQGTTVTVSS 123


RESULT 15
US-10-309-762-8
; Sequence 8, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-8

  Query Match             83.5%;  Score 508.5;  DB 15;  Length 125;
  Best Local Similarity   79.2%;  Pred. No. 1.1e-40;
  Matches   95;  Conservative   12;  Mismatches    6;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
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Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDGY--TLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||     | ||    |||||||:|||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARTYYDILTGYPDAFDIWGQGTMVTVSS 125


Search completed: August  8, 2004, 12:43:20
Job time : 39.5182 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	499	81.9	473	3	US-09-049-672A-4	Sequence 4, Appli
2	496	81.4	172	4	US-09-472-087-7	Sequence 7, Appli
3	496	81.4	172	4	US-09-472-087-86	Sequence 86, Appl
4	482	79.1	487	4	US-09-800-729-145	Sequence 145, App
5	471.5	77.4	119	1	US-08-360-125-5	Sequence 5, Appli
6	471.5	77.4	119	2	US-08-450-578-5	Sequence 5, Appli
7	471.5	77.4	119	2	US-09-017-628-5	Sequence 5, Appli
8	471.5	77.4	119	2	US-09-014-880-5	Sequence 5, Appli
9	471.5	77.4	119	4	US-09-025-769B-39	Sequence 39, Appl
10	471.5	77.4	119	4	US-09-025-769B-65	Sequence 65, Appl
11	471.5	77.4	119	4	US-08-450-363-5	Sequence 5, Appli
12	466	76.5	122	1	US-08-360-125-11	Sequence 11, Appl
13	466	76.5	122	2	US-08-450-578-11	Sequence 11, Appl
14	466	76.5	122	2	US-09-017-628-11	Sequence 11, Appl
15	466	76.5	122	2	US-09-014-880-11	Sequence 11, Appl
16	466	76.5	122	4	US-08-450-363-11	Sequence 11, Appl
17	455	74.7	118	4	US-09-025-769B-25	Sequence 25, Appl
18	453	74.4	118	3	US-08-545-809A-116	Sequence 116, App
19	446.5	73.3	250	4	US-10-039-785-50	Sequence 50, Appl
20	445	73.1	244	4	US-08-918-148-79	Sequence 79, Appl
21	442.5	72.7	142	2	US-08-480-774A-2	Sequence 2, Appli
22	438	71.9	278	3	US-09-260-527-3	Sequence 3, Appli
23	429.5	70.5	119	2	US-08-652-816A-10	Sequence 10, Appl
24	429	70.4	150	4	US-09-582-337-14	Sequence 14, Appl
25	427	70.1	118	4	US-09-343-698-6	Sequence 6, Appli
26	427	70.1	118	4	US-08-325-955-6	Sequence 6, Appli
27	425.5	69.9	476	3	US-08-487-550-12	Sequence 12, Appl
28	425.5	69.9	476	4	US-09-526-098-12	Sequence 12, Appl
29	424	69.6	118	3	US-08-545-809A-142	Sequence 142, App
30	422.5	69.4	98	1	US-08-478-039-75	Sequence 75, Appl
31	422.5	69.4	98	1	US-08-476-349A-75	Sequence 75, Appl
32	422	69.3	126	1	US-08-276-852-142	Sequence 142, App
33	422	69.3	126	1	US-08-899-575-142	Sequence 142, App
34	422	69.3	126	1	US-08-899-575-142	Sequence 142, App
35	422	69.3	126	5	PCT-US95-08743-142	Sequence 142, App
36	420.5	69.0	124	1	US-08-478-039-78	Sequence 78, Appl
37	420.5	69.0	124	1	US-08-476-349A-78	Sequence 78, Appl
38	420	69.0	832	3	US-08-630-820-7	Sequence 7, Appli
39	420	69.0	832	4	US-09-273-453-7	Sequence 7, Appli
40	419.5	68.9	219	4	US-09-460-384-37	Sequence 37, Appl
41	418.5	68.7	96	3	US-08-851-362D-27	Sequence 27, Appl
42	418.5	68.7	117	3	US-08-851-362D-44	Sequence 44, Appl
43	418.5	68.7	123	4	US-08-793-450-4	Sequence 4, Appli
44	418.5	68.7	472	4	US-08-793-450-8	Sequence 8, Appli
45	418	68.6	244	4	US-10-039-785-44	Sequence 44, Appl

ALIGNMENTS

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RESULT 1
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Tang, Y. Tom
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Baughn, Mariah R.
;    TITLE OF INVENTION:  HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,672A
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0497 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  473 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  PANCTUT01
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;      CLONE:  1513264
US-09-049-672A-4

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  Best Local Similarity   78.2%;  Pred. No. 3.6e-43;
  Matches   93;  Conservative   13;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
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Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLD------GYTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||| |       | :|:||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143


RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-7

  Query Match             81.4%;  Score 496;  DB 4;  Length 172;
  Best Local Similarity   79.8%;  Pred. No. 2.2e-43;
  Matches   91;  Conservative   12;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLK 62
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Qy         63 SRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YTLDIWGQGTLVTVSS 114
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Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-86

  Query Match             81.4%;  Score 496;  DB 4;  Length 172;
  Best Local Similarity   79.8%;  Pred. No. 2.2e-43;
  Matches   91;  Conservative   12;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSLK 62
              |||||||||:| |||:| |||||| |||:||||||||||||||||||||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG--YTLDIWGQGTLVTVSS 114
              ||: :|||||:|:|||:|:|||||||||||||| |   | :|:||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 4
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 145
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-800-729-145

  Query Match             79.1%;  Score 482;  DB 4;  Length 487;
  Best Local Similarity   74.8%;  Pred. No. 2e-41;
  Matches   92;  Conservative   12;  Mismatches    9;  Indels   10;  Gaps    2;

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Db         25 ESGPGLVKPSETLSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYISYNGVTYYNPSL 84

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR-----LDGYTL-----DIWGQGTLVT 111
              |||: :|||||:|:|||||:|||||||||||||:       ||| |     | |||| |||
Db         85 KSRVTISVDTSQNQFSLRLSSVTAADTAVYYCAKDHRATRDGYQLEYRGFDYWGQGILVT 144

Qy        112 VSS 114
              |||
Db        145 VSS 147


RESULT 5
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
;  GENERAL INFORMATION:
;     APPLICANT:  Saiko HOSOKAWA
;     APPLICANT:  Toshiaki TAGAWA
;     APPLICANT:  Yoko HIRAKAWA
;     APPLICANT:  No. 5767246ihiko ITO
;     APPLICANT:  Kazuhiro NAGAIKE
;     TITLE OF INVENTION:  Human Monoclonal Antibody
;     TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;     TITLE OF INVENTION:  Cell Membrane
```

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;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,125
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5

  Query Match             77.4%;  Score 471.5;  DB 1;  Length 119;
  Best Local Similarity   75.9%;  Pred. No. 4.6e-41;
  Matches   88;  Conservative   16;  Mismatches    7;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| | |:||:|||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDGYTLDIWGQGTLVTVSS 114
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Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRG--ADYWGQGTMVTVSS 119


RESULT 6
US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 5837845ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,578
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
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;       STRAIN:
;       INDIVIDUAL ISOLATE:
;       DEVELOPMENTAL STAGE:
;       HAPLOTYPE:
;       TISSUE TYPE:
;       CELL TYPE:  Hybridoma producing human
;       CELL TYPE:  antibody GAH
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

  Query Match             77.4%;  Score 471.5;  DB 2;  Length 119;
  Best Local Similarity   75.9%;  Pred. No. 4.6e-41;
  Matches   88;  Conservative   16;  Mismatches    7;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| | |:||:||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDGYTLDIWGQGTLVTVSS 114
              |||: :|:|||:::|||:|:|:||||||||||    || |    | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRG--ADYWGQGTMVTVSS 119


RESULT 7
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
;  APPLICANT: HOSOKAWA, Saiko
;  APPLICANT: TAGAWA, Toshiaki
;  APPLICANT: HIRAKAWA, Yoko
;  APPLICANT: ITO, No. 5990287ihiko
;  APPLICANT: NAGAIKE, Kazuhiro
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
;  TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;  FILE REFERENCE: 177/527361KH
;  CURRENT APPLICATION NUMBER: US/09/017,628
;  CURRENT FILING DATE: 1998-02-02
;  EARLIER APPLICATION NUMBER: 08/360,125
;  EARLIER FILING DATE: 1994-12-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

  Query Match             77.4%;  Score 471.5;  DB 2;  Length 119;
  Best Local Similarity   75.9%;  Pred. No. 4.6e-41;
  Matches   88;  Conservative   16;  Mismatches    7;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| | |:||:||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDGYTLDIWGQGTLVTVSS 114
              |||: :|:|||:::|||:|:|:||||||||||    || |    | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRG--ADYWGQGTMVTVSS 119


RESULT 8
US-09-014-880-5
; Sequence 5, Application US/09014880
; Patent No. 5990297
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA et al.
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
;    TITLE OF INVENTION:  BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack, L.L.P.
;      STREET:  2033 K Street, N.W., #800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/014,880
;      FILING DATE:  January 28, 1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/450,578
;      FILING DATE:  May 25, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-721-8200
;      TELEFAX:  202-721-8250
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
US-09-014-880-5

  Query Match             77.4%;  Score 471.5;  DB 2;  Length 119;
  Best Local Similarity   75.9%;  Pred. No. 4.6e-41;
  Matches   88;  Conservative   16;  Mismatches    7;  Indels    5;  Gaps    2;
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Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:||||:| |||||| | |:||:||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDGYTLDIWGQGTLVTVSS 114
              |||: :|:|||:::|||:|:|:||||||||||    || |   | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRG--ADYWGQGTMVTVSS 119


RESULT 9
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-39

  Query Match             77.4%;  Score 471.5;  DB 4;  Length 119;
  Best Local Similarity   77.6%;  Pred. No. 4.6e-41;
  Matches   90;  Conservative   12;  Mismatches    9;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| |||||||||||:||:| |||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 63

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG---YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||||   |   | :| ||||||||||
Db         64 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119


RESULT 10
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-65

  Query Match             77.4%;  Score 471.5;  DB 4;  Length 119;
  Best Local Similarity   77.6%;  Pred. No. 4.6e-41;
  Matches   90;  Conservative   12;  Mismatches    9;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  |||||||| |||||||||||:||:| |||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 63

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDG---YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||||   |   | :| ||||||||||
Db         64 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119


RESULT 11
US-08-450-363-5
; Sequence 5, Application US/08450363
; Patent No. 6436434
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 6436434ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
```

```
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/450,363
;       FILING DATE:  May 25, 1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/360,125
;       FILING DATE:  December 20, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/905,534
;       FILING DATE:  June 29, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warren M. Cheek, Jr.
;       REGISTRATION NUMBER:  33,367
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-8850
;       TELEFAX:
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:
;     ANTI-SENSE:
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:
;       STRAIN:
;       INDIVIDUAL ISOLATE:
;       DEVELOPMENTAL STAGE:
;       HAPLOTYPE:
;       TISSUE TYPE:
;       CELL TYPE:  Hybridoma producing human
;       CELL TYPE:  antibody GAH
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-5

  Query Match             77.4%;  Score 471.5;  DB 4;  Length 119;
  Best Local Similarity   75.9%;  Pred. No. 4.6e-41;
  Matches   88;  Conservative   16;  Mismatches    7;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||:| |||||| | |:||:||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCA---RLDGYTLDIWGQGTLVTVSS 114
              |||: :|:|||:::|||:|:|:||||||||||    || |   | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRG--ADYWGQGTMVTVSS 119


RESULT 12
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 5767246ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,125
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
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;       CELL TYPE:  Hybridoma producing human antibody 1-3-1
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

  Query Match             76.5%;  Score 466;  DB 1;  Length 122;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-40;
  Matches   88;  Conservative   13;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||| |||| |||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDG--YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||    |  | :|:|||| ||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 13
US-08-450-578-11
; Sequence 11, Application US/08450578
; Patent No. 5837845
;  GENERAL INFORMATION:
;     APPLICANT:  Saiko HOSOKAWA
;     APPLICANT:  Toshiaki TAGAWA
;     APPLICANT:  Yoko HIRAKAWA
;     APPLICANT:  No. 5837845ihiko ITO
;     APPLICANT:  Kazuhiro NAGAIKE
;     TITLE OF INVENTION:  Human Monoclonal Antibody
;     TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;     TITLE OF INVENTION:  Cell Membrane
;     NUMBER OF SEQUENCES:  42
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wenderoth, Lind & Ponack
;       STREET:  805 Fifteenth Street, N.W., #700
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/450,578
;       FILING DATE:  May 25, 1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/360,125
;       FILING DATE:  December 20, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/905,534
;       FILING DATE:  June 29, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warren M. Cheek, Jr.
;       REGISTRATION NUMBER:  33,367
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-8850
;       TELEFAX:
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  122 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:
;     ANTI-SENSE:
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:
;       STRAIN:
;       INDIVIDUAL ISOLATE:
;       DEVELOPMENTAL STAGE:
;       HAPLOTYPE:
;       TISSUE TYPE:
;       CELL TYPE:  Hybridoma producing human antibody 1-3-1
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

  Query Match             76.5%;  Score 466;  DB 2;  Length 122;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-40;
  Matches   88;  Conservative   13;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||| |||| |||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDG--YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||    |  | :|:|||| ||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 14
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US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
;  APPLICANT: HOSOKAWA, Saiko
;  APPLICANT: TAGAWA, Toshiaki
;  APPLICANT: HIRAKAWA, Yoko
;  APPLICANT: ITO, No. 5990287ihiko
;  APPLICANT: NAGAIKE, Kazuhiro
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
;  TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;  FILE REFERENCE: 177/527361KH
;  CURRENT APPLICATION NUMBER: US/09/017,628
;  CURRENT FILING DATE: 1998-02-02
;  EARLIER APPLICATION NUMBER: 08/360,125
;  EARLIER FILING DATE: 1994-12-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;    LENGTH: 122
;    TYPE: PRT
;    ORGANISM: Unknown
;    FEATURE:
;    OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

  Query Match             76.5%;  Score 466;  DB 2;  Length 122;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-40;
  Matches   88;  Conservative   13;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||| |||| |||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDG--YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||    |  | :|:||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 15
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA et al.
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
;    TITLE OF INVENTION:  BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack, L.L.P.
;      STREET:  2033 K Street, N.W., #800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/014,880
;      FILING DATE:  January 28, 1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/450,578
;      FILING DATE:  May 25, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-721-8200
;      TELEFAX:  202-721-8250
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      CELL TYPE:  Hybridoma producing human antibody 1-3-1
US-09-014-880-11

  Query Match             76.5%;  Score 466;  DB 2;  Length 122;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-40;
  Matches   88;  Conservative   13;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||::||||:| |||||| |  ||| |||| |||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRIAMSVDTSENKFSLRLNSVTAADTAVYYCAR--LDG--YTLDIWGQGTLVTVSS 114
              |||: :|||||:|:|||:|:|||||||||||||    |  | :|:||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


Search completed: August  8, 2004, 12:20:23
Job time : 14.6455 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 10.0182 Seconds
(without alignments)
1094.593 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	499.5	81.4	135	2	S78051	Ig heavy chain pre
2	495.5	80.7	147	2	S13519	Ig heavy chain V r
3	487	79.3	130	2	S30534	Ig heavy chain V r
4	480.5	78.3	121	2	S44113	Ig heavy chain V r
5	478.5	77.9	140	2	I37782	Ig variable region
6	477.5	77.8	146	2	S09710	Ig heavy chain V r
7	474.5	77.3	116	2	S37456	Ig mu chain - huma
8	474.5	77.3	130	2	S31690	Ig heavy chain V r
9	474	77.2	122	2	S69912	Ig V-D-J region (N
10	473.5	77.1	128	2	S31514	Ig heavy chain - h
11	472.5	77.0	127	2	S19668	Ig heavy chain V r
12	469	76.4	137	2	S31676	Ig heavy chain V r
13	468.5	76.3	123	2	S30530	Ig heavy chain V r
14	465.5	75.8	155	2	S31511	Ig heavy chain - h
15	463.5	75.5	155	2	S31512	Ig heavy chain - h
16	462	75.2	139	2	S31586	Ig heavy chain V r
17	460.5	75.0	146	2	S09711	Ig heavy chain V r
18	460	74.9	145	2	S78055	Ig heavy chain pre
19	459.5	74.8	109	2	PH1673	Ig heavy chain V r
20	457	74.4	110	2	S44110	Ig heavy chain V-D
21	455	74.1	99	2	S26803	Ig heavy chain V r
22	454	73.9	139	2	A41287	Ig heavy chain pre
23	453	73.8	99	2	S26801	Ig heavy chain V r
24	452	73.6	129	2	S44114	Ig heavy chain V r
25	450	73.3	99	2	S26802	Ig heavy chain V r
26	450	73.3	135	2	S31604	Ig heavy chain V r
27	447	72.8	118	2	S20780	Ig heavy chain V r
28	446	72.6	99	2	S12418	Ig heavy chain V r
29	444.5	72.4	139	2	S31696	Ig heavy chain V r
30	443	72.1	118	2	A26340	Ig heavy chain pre
31	442.5	72.1	140	2	A49045	Ig heavy chain V r
32	441.5	71.9	132	2	A38911	Ig heavy chain V r
33	441	71.8	99	2	S26800	Ig heavy chain V r
34	441	71.8	126	2	S47010	Ig heavy chain V4.
35	440.5	71.7	129	1	D2HUWA	Ig heavy chain V-I
36	440	71.7	97	2	PL0118	Ig heavy chain V-I
37	440	71.7	99	2	S26899	Ig heavy chain V r
38	439.5	71.6	98	2	S12421	Ig heavy chain V r
39	439.5	71.6	140	2	A24770	hypothetical hybri
40	439	71.5	140	2	S78052	Ig heavy chain pre
41	438.5	71.4	123	2	S30529	Ig heavy chain V r
42	438	71.3	120	2	PT0370	Ig mu chain precur
43	437	71.2	124	2	S31684	Ig heavy chain V r
44	435.5	70.9	134	2	S54906	Ig heavy chain V r
45	434.5	70.8	98	2	S26902	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S78051
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78051; S23716
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Molecule type: mRNA
A;Residues: 1-135 <HAR>
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23716
A;Molecule type: mRNA
A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 499.5; DB 2; Length 135;
Best Local Similarity 79.7%; Pred. No. 9.3e-38;
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

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Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||:|||||||||||||  | :|| |:||||||||||||:||:||||:||||
Db         18 ESGPGLVKPSETLSLTCTVSGGSISRGSHYWGWIRQPPGKGLEWIGSIYYSGNTYFNPSL 77

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGYTLDN---WGQGTLVTVSS 114
              |||:|:|||||| |||:|:||||||||||||||   | ||||    ||||| |||||
Db         78 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGTTVTVSS 135
```

RESULT 2
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

  Query Match             80.7%;  Score 495.5;  DB 2;  Length 147;
  Best Local Similarity   80.2%;  Pred. No. 2.3e-37;
  Matches   93;  Conservative    9;  Mismatches   11;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||| |:|||||||||||:||:||:|||||||
Db         32 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 91

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||||||||     |   | ||||||||||
Db         92 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPLLWFGELFDYWGQGTLVTVSS 147


RESULT 3
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             79.3%;  Score 487;  DB 2;  Length 130;
  Best Local Similarity   76.0%;  Pred. No. 1.2e-36;
  Matches   95;  Conservative    7;  Mismatches   11;  Indels   12;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| || |||||:||| |||||||| || ||:| |||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG------YT------LDNWGQGTL 109
              |||:|:|||||||  |||:|:|||||||||||||  |       ||       | |||||:
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIWGQGTM 125

Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130


RESULT 4
S44113
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <HAW>
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             78.3%;  Score 480.5;  DB 2;  Length 121;
  Best Local Similarity   78.4%;  Pred. No. 4.1e-36;
  Matches   91;  Conservative    9;  Mismatches   13;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| | |  ||| | |||||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGY--TLDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||  ||||:| | ||    | | |||||||||
Db         66 KSRVTLSVDTSKNQFSLKLSSVTAADTGVYYCSRLSGGYYSDFDYWSQGTLVTVSS 121


RESULT 5
I37782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

  Query Match             77.9%;  Score 478.5;  DB 2;  Length 140;
  Best Local Similarity   78.8%;  Pred. No. 7.2e-36;
  Matches   93;  Conservative    9;  Mismatches    9;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| |  |||||:|||||||||||| ||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||||||||| :     |   | ||||||||||
Db         83 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTLVTVSS 140


RESULT 6
S09710
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S09710
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09710
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

  Query Match             77.8%;  Score 477.5;  DB 2;  Length 146;
  Best Local Similarity   73.2%;  Pred. No. 9.3e-36;
  Matches   90;  Conservative   13;  Mismatches    9;  Indels   11;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:||||||:|||||: ||| || |||||||||||||:|::||:|||||||
Db         25 ESGPGLVKPSETLSLTCSVSGGSVSSGGLYWGWVRQPPGKGLEWIGSIFYSGSTYYNPSL 84
```

```
Qy          62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGY----------TLDNWGQGTLVT 111
               |||:|:|||| ||:|||:|:|||||||||||| |  ||          :| ||||| ||
Db          85 KSRVTISVDTLKNNFSLKLSSVTAADTAVYYCTR-PGYGDTSVRKRVWNMDLWGQGTTVT 143

Qy         112 VSS 114
               |||
Db         144 VSS 146
```

RESULT 7
S37456
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

  Query Match   77.3%; Score 474.5; DB 2; Length 116;
  Best Local Similarity   77.8%; Pred. No. 1.3e-35;
  Matches   91; Conservative   10; Mismatches   7; Indels   9; Gaps   2;

```
Qy           6 GLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKSRI 65
               |||||||||||||||||||| ||||||||:|| ||||||||| ||:||:|||||||||:
Db           1 GLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRV 60

Qy          66 TMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT--------LDNWGQGTLVTVSS 114
               |:||||||| |||:|:|||||||||||||  ||:        :| ||:|| |||||
Db          61 TISVDTSKNQFSLKLSSVTAADTAVYYCARG-GYSYGYYYYYYYMDVWGKGTTVTVSS 116
```

RESULT 8
S31690
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

  Query Match   77.3%; Score 474.5; DB 2; Length 130;
  Best Local Similarity   76.2%; Pred. No. 1.5e-35;
  Matches   93; Conservative   7; Mismatches   11; Indels   11; Gaps   2;

```
Qy           2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
               ||||||||||:|||||||||||||| |  ||||| |||||||||||| ||:||:| |||||
Db          11 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWSRQPPGKGLEWIGYIYYSGSTNYNPSL 68

Qy          62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG---------YTLDNWGQGTLVTV 112
               |||:|:|||||||| |||:|:|||||||||||||||            |  | |||||||||
Db          69 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSSVLLWFGELLYYFDYWGQGTLVTV 128

Qy         113 SS 114
               ||
Db         129 SS 130
```

RESULT 9
S69912
Ig V-D-J region (ND) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of mult
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69912
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: EMBL:Z33398; NID:g871347; PIDN:CAA83849.1; PID:g887460
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence ar
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match   77.2%; Score 474; DB 2; Length 122;
  Best Local Similarity   76.9%; Pred. No. 1.6e-35;
  Matches   90; Conservative   11; Mismatches   12; Indels   4; Gaps   1;

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Qy           2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
               |||||||||||||||||:|||||| | |::|:|:|| |||||||||||| ||::||||||
Db           6 ESGPGLVKPSQTLSLTCSVSGGSISSDGHFWNWIRQHPGKGLEWIGNIYFSGSSYYNPSL 65

Qy          62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS----DGYTLDNWGQGTLVTVSS 114
               ||||::|||||| |||| ||||||||||:|||        | || ||||||| :||
Db          66 KSRISISVDTSKNQFSLRLKSVTAADTAVYFCARGFFFRGTYGLDTWGQGTLVRLSS 122
```

RESULT 10
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

  Query Match   77.1%; Score 473.5; DB 2; Length 128;
  Best Local Similarity   77.6%; Pred. No. 1.8e-35;
  Matches   90; Conservative   9; Mismatches   14; Indels   3; Gaps   1;

```
Qy           2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
               |||||||:|||||||||||||||| |||:||||:|| ||  |||| :|| ||:||||| |
Db          13 ESGPGLVRPSQTLSLTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIYFSGSTYYNPFL 72

Qy          62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR---SDGYTLDNWGQGTLVTVSS 114
               |||: :|||||:| |||||||| ||||||||||    : ||  | ||||||||||
Db          73 KSRVIISVDTSENQFSLRLTSVTPADTAVYYCARIGYNFGYGFDPWGQGTLVTVSS 128
```

RESULT 11
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000

```
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118,'E',120-121,'T',123-126,'F' <JON>
A;Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             77.0%;  Score 472.5;  DB 2;  Length 127;
  Best Local Similarity   73.0%;  Pred. No. 2.2e-35;
  Matches   89;  Conservative   12;  Mismatches   12;  Indels    9;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              :|| |||||||||||||:||| || |||| |||:||| ||||||||:::|||| |||||||
Db          6 QSGSGLVKPSQTLSLTCSVSGDSISSGGYSWSWIRQPSGKGLEWIGSVHHSGPTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG---------YTLDNWGQGTLVTV 112
              |||:|||||||| |||:| ||||||||:|:|||  |          | :| ||:||||||
Db         66 KSRVTMSVDTSKNQFSLKLKSVTAADTAMYFCAREGGSTWRSLYKHYYMDVWGKGTLVTV 125

Qy        113 SS 114
              ||
Db        126 SS 127


RESULT 12
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

  Query Match             76.4%;  Score 469;  DB 2;  Length 137;
  Best Local Similarity   80.0%;  Pred. No. 5e-35;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| |  |||||:||| |||||||| || ||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              |||:|||||||| |||:|:|||||||||||||||     | :| ||||| |||||
Db         83 KSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDAPLMYGMDVWGQGTTVTVSS 137


RESULT 13
S30530
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S30530
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MAR>
A;Cross-references: EMBL:Z18316
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             76.3%;  Score 468.5;  DB 2;  Length 123;
  Best Local Similarity   75.6%;  Pred. No. 4.9e-35;
  Matches   90;  Conservative   11;  Mismatches   11;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||| || | |||| |:|||||||||||:::|||::||||||
Db          6 ESGPGLVKPSETLSLTCTVSGYSI-SSGYYWGWIRQPPGKGLEWIGSMFHSGSSYYNPSL 64

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR------SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:| |||||||||||||      :     | ||||||||||
Db         65 KSRVTISVDTSKNQFSLQLRSVTAADTAVYYCARGRYCSSTSCNWFDPWGQGTLVTVSS 123


RESULT 14
S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A;Reference number: S31509
A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

  Query Match             75.8%;  Score 465.5;  DB 2;  Length 155;
  Best Local Similarity   74.2%;  Pred. No. 1.2e-34;
  Matches   89;  Conservative   11;  Mismatches   11;  Indels    9;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| |  |||||:||||||||||| ||::|:  ||| |
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPL 95

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-------YTLDNWGQGTLVTVSS 114
              |||:|:||||||| |||:::|||||||||||||||  |       | :| ||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTVTVSS 155


RESULT 15
S31512
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A;Reference number: S31509
A;Accession: S31512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
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A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

  Query Match             75.5%;  Score 463.5;  DB 2;  Length 155;
  Best Local Similarity   73.3%;  Pred. No. 1.8e-34;
  Matches   88;  Conservative   12;  Mismatches   11;  Indels    9;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| |  |||||:|||||||||||| ||::|:  ||| :
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPI 95

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-------YTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:::|||||||||||||||  |       | :| ||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYVYYGMDVWGQGTTVTVSS 155


Search completed: August  8, 2004, 12:18:54
Job time : 11.0182 secs
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 6.21818 Seconds
(without alignments)
954.620 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	440.5	71.7	129	1	HV2F_HUMAN	P01824 homo sapien
2	417	67.9	146	1	HV2I_HUMAN	P06331 homo sapien
3	381.5	62.1	117	1	HV2G_HUMAN	P01825 homo sapien
4	363.5	59.2	137	1	HV46_MOUSE	P01822 mus musculu
5	352.5	57.4	144	1	HV43_MOUSE	P01819 mus musculu
6	347.5	56.6	113	1	HV47_MOUSE	P01823 mus musculu
7	338.5	55.1	116	1	HV61_MOUSE	P18532 mus musculu
8	335	54.6	117	1	HV62_MOUSE	P18533 mus musculu
9	332.5	54.2	116	1	HV60_MOUSE	P18531 mus musculu
10	325	52.9	135	1	HV02_XENLA	P20957 xenopus lae
11	314	51.1	120	1	HV2B_HUMAN	P01815 homo sapien
12	295.5	48.1	119	1	HV2C_HUMAN	P01816 homo sapien
13	294	47.9	147	1	HV2H_HUMAN	P04438 homo sapien
14	288.5	47.0	136	1	HV01_XENLA	P20956 xenopus lae
15	288	46.9	115	1	HV44_MOUSE	P01820 mus musculu
16	288	46.9	119	1	HV40_MOUSE	P01810 mus musculu
17	287.5	46.8	125	1	HV2D_HUMAN	P01817 homo sapien
18	286.5	46.7	121	1	HV2E_HUMAN	P01818 homo sapien
19	285.5	46.5	117	1	HV2B_RABIT	P01828 oryctolagus
20	283	46.1	126	1	HV2A_HUMAN	P01814 homo sapien
21	282	45.9	114	1	HV3B_HUMAN	P01763 homo sapien
22	281	45.8	122	1	HV3A_HUMAN	P01762 homo sapien
23	281	45.8	122	1	HV3G_HUMAN	P01768 homo sapien
24	278	45.3	119	1	HV37_MOUSE	P01807 mus musculu
25	277	45.1	116	1	HV05_CARAU	P19181 carassius a
26	276.5	45.0	121	1	HV3J_HUMAN	P01771 homo sapien
27	276	45.0	119	1	HV38_MOUSE	P01808 mus musculu
28	275	44.8	116	1	HV45_MOUSE	P01821 mus musculu
29	274.5	44.7	142	1	HV01_RAT	P01805 rattus norv
30	274	44.6	136	1	HV2C_RABIT	P01829 oryctolagus
31	273.5	44.5	117	1	HV41_MOUSE	P01811 mus musculu
32	273.5	44.5	117	1	HV42_MOUSE	P01812 mus musculu
33	272	44.3	114	1	HV2A_RABIT	P01827 oryctolagus
34	271	44.1	122	1	HV3H_HUMAN	P01769 homo sapien
35	267	43.5	118	1	HV51_MOUSE	P06330 mus musculu
36	267	43.5	139	1	HV07_MOUSE	P01751 mus musculu
37	265.5	43.2	117	1	HV12_MOUSE	P01756 mus musculu
38	264.5	43.1	115	1	HV3D_HUMAN	P01765 homo sapien
39	264.5	43.1	117	1	HV13_MOUSE	P01757 mus musculu
40	264	43.0	122	1	HV20_MOUSE	P01789 mus musculu
41	262.5	42.8	115	1	HV3F_HUMAN	P01767 homo sapien
42	262.5	42.8	117	1	HV02_CANFA	P01785 canis famil
43	261	42.5	116	1	HV3T_HUMAN	P01781 homo sapien
44	261	42.5	126	1	HV3K_HUMAN	P01772 homo sapien
45	260	42.3	120	1	HV50_MOUSE	P06329 mus musculu

ALIGNMENTS

RESULT 1
HV2F_HUMAN
ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01825; 7FAB.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;
Best Local Similarity 65.1%; Pred. No. 1.7e-38;
Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||| |||| ||  |||| |:||||||||||| :|::|: ||||||
Db          6 ESGPGLVKPSETLSLTCIVSGGPIRRTGYYWGWIRQPPGKGLEWIGGVYYTGSIYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR------------SDGYTLDNWGQGT 108
              : |:|:|||||:| ||| | |::|||||:|||||              ||  :| |||||
Db         66 RGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYYDIGTGSDDG--IDVWGQGT 123

Qy        109 LVTVSS 114
               | |||
Db        124 TVHVSS 129
```

RESULT 2

```
HV2I_HUMAN
ID   HV2I_HUMAN     STANDARD;      PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146       IG HEAVY CHAIN V-II REGION ARH-77.
FT   DOMAIN       20    117       V SEGMENT.
FT   DOMAIN      118    127       D SEGMENT.
FT   DOMAIN      128    146       J SEGMENT.
FT   DISULFID     42    115       BY SIMILARITY.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16228 MW;  8D7FD52BB218171F CRC64;

  Query Match             67.9%;  Score 417;  DB 1;  Length 146;
  Best Local Similarity   68.6%;  Pred. No. 5.1e-36;
  Matches   83;  Conservative   10;  Mismatches   16;  Indels   12;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||||||:|||||| | |||    ||||||:|||||:|||||| | |||:| |  ||||
Db         28 GAGLVKPSETLSLTCAVFGGSF--SGYYWSWIRQPPGRGLEWIGEINHSGSTNYKTSLKS 85

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCARS---DG-------YTLDNWGQGTLVTVS 113
              |:|:|:||||| |||:|:|||||||||||||     |       | :| |||| ||||
Db         86 RVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWNDVDYYYGMDVWGQGTTVTVS 145

Qy        114 S 114
              |
Db        146 S 146


RESULT 3
HV2G_HUMAN
ID   HV2G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01825;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region NEWM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77242302; PubMed=407927;
RA   Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT   "Amino acid sequence of the VH region of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 16:3412-3420(1977).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX   MEDLINE=78066916; PubMed=618887;
RA   Saul F.A., Amzel L.M., Poljak R.J.;
RT   "Preliminary refinement and structural analysis of the Fab fragment
RT   from human immunoglobulin new at 2.0-A resolution.";
RL   J. Biol. Chem. 253:585-597(1978).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90404; G1HUNM.
DR   PDB; 7FAB; 31-JAN-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    111       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   TURN         30     31
FT   STRAND       33     39
FT   TURN         41     42
FT   STRAND       46     51
FT   TURN         53     54
FT   STRAND       57     59
FT   HELIX        61     63
FT   TURN         64     66
FT   STRAND       67     72
FT   TURN         73     76
FT   STRAND       77     82
FT   HELIX        87     89
FT   STRAND       91     98
FT   STRAND      104    107
FT   STRAND      111    115
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12790 MW;  2DA47B509562D237 CRC64;

  Query Match             62.1%;  Score 381.5;  DB 1;  Length 117;
  Best Local Similarity   65.8%;  Pred. No. 1.8e-32;
  Matches   75;  Conservative   17;  Mismatches   19;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              :||||||:|||||||||||||| :  :   |::|||||||:|||||| ::: | :     |
Db          6 QSGPGLVRPSQTLSLTCTVSGSTFSND--YYTWVRQPPGRGLEWIGYVFYHGTSDDTTPL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS-DGYTLDNWGQGTLVTVSS 114
              :||:|| |||||| |||||:|||||||||||||:     :| ||||:||||||
Db         64 RSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLIAGCIDVWGQGSLVTVSS 117


RESULT 4
HV46_MOUSE
ID   HV46_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=89238351; PubMed=2497341;
RA   Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT   "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT   gene segment.";
RL   Mol. Immunol. 26:431-434(1989).
RN   [2]
RP   SEQUENCE OF 1-31.
RX   MEDLINE=78094475; PubMed=414225;
RA   Jilka R.L., Pestka S.;
RT   "Amino acid sequence of the precursor region of MOPC-315 mouse
RT   immunoglobulin heavy chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN   [3]
RP   SEQUENCE OF 1-21.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [4]
RP   SEQUENCE OF 19-136.
RX   MEDLINE=74170779; PubMed=4524622;
RA   Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT   "Amino-acid sequence of the variable region of the heavy (alpha)
RT   chain of a mouse myeloma protein with anti-hapten activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN   [5]
RP   REVISION TO 53.
RX   MEDLINE=77244979; PubMed=268248;
RA   Hood L., Margolies M.N., Givol D., Zakut R.;
RL   Unpublished results, cited by:
RL   Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL   Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC   -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M27638; AAA61337.1; -.
DR   EMBL; X07880; CAA30727.1; -.
DR   PIR; PL0102; AVMS35.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    137       IG HEAVY CHAIN V REGION MOPC 315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DOMAIN      117    126       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      127    137       FRAMEWORK-4.
FT   DISULFID     40    114       BY SIMILARITY.
FT   CONFLICT     15     15       G -> GG (IN REF. 1; CAA30727).
FT   CONFLICT     15     15       G -> H (IN REF. 2).
FT   CONFLICT     77     78       GY -> YG (IN REF. 4).
FT   CONFLICT    102    102       N -> D (IN REF. 4).
FT   CONFLICT.   123    123       MISSING (IN REF. 4).
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15399 MW;  FB3828304C2B81DC CRC64;

  Query Match             59.2%;  Score 363.5;  DB 1;  Length 137;
  Best Local Similarity   60.9%;  Pred. No. 1.5e-30;
  Matches   70;  Conservative   18;  Mismatches   24;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||:|:| || | ||:|:|:|| ||  |||:|.| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYFWNWIRQFPGNKLEWLGFIKYDGSNGYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              |:|:::: |||:| | |:| |||  ||| ||||  :   |  | ||||| :||||
Db         83 KNRVSITRDTSENQFFLKLNSVTTEDTATYYCAGDNDHLYYFDYWGQGTTLTVSS 137


RESULT 5
HV43_MOUSE
ID   HV43_MOUSE     STANDARD;      PRT;   144 AA.
AC   P01819;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOPC 141 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC       DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00768; CAA24149.1; -.
DR   PIR; A02094; G2MS14.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    144       IG HEAVY CHAIN V REGION MOPC 141.
FT   DOMAIN       20    130       IG-LIKE.
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15759 MW;  8E47A7CB3706D30A CRC64;

  Query Match             57.4%;  Score 352.5;  DB 1;  Length 144;
  Best Local Similarity   59.8%;  Pred. No. 2.2e-29;
  Matches   73;  Conservative   16;  Mismatches   22;  Indels   11;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||| |||:||:|||||| |:   ||  :|||||||||||:| |: :|:| || :|
Db         25 ESGPGLVAPSQSLSITCTVSGFSLT--GYGVNWVRQPPGKGLEWLGTIWGNGSTDYNSTL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA--------RSDGY-TLDNWGQGTLVTV 112
              |||:|:: | ||:   |:: |:  ||| ||||         ||| | ||| ||||| |||
Db         83 KSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSIYYYGRSDKYFTLDYWGQGTSVTV 142

Qy        113 SS 114
              ||
Db        143 SS 144
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RESULT 6
HV47_MOUSE
ID   HV47_MOUSE     STANDARD;      PRT;   113 AA.
AC   P01823;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-60.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=84024551; PubMed=6414509;
RA   Juszczak E.C., Margolies M.N.;
RT   "Amino acid sequence of the heavy chain variable region from the A/J
RT   mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
RT   idiotype.";
RL   Biochemistry 22:4291-4296(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC       MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC       IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC       STRAIN A/J MICE.
DR   PIR; A02098; G2MS60.
DR   PDB; 1J1O; 18-FEB-03.
DR   PDB; 1J1P; 18-FEB-03.
DR   PDB; 1J1X; 18-FEB-03.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   NON_TER      113    113
SQ   SEQUENCE   113 AA;  12734 MW;  38DC0E0E3F5075B7 CRC64;

  Query Match             56.6%;  Score 347.5;  DB 1;  Length 113;
  Best Local Similarity   61.9%;  Pred. No. 5.5e-29;
  Matches   70;  Conservative   15;  Mismatches   23;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||| |||||||||||||:|:| || |   ||:|:|: ||  || :| | :||:|||||||
Db          6 ESGPSLVKPSQTLSLTCSVTGDSITSD--YWNWIRKFPGNKLEHMGYISYSGSTYYNPSL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||::: ||||| : |:| |||: ||| |||           ||||||||||:
Db         64 KSRISITRDTSKNQYYLQLNSVTSEDTATYYCT---SLRFAYWGQGTLVTVSA 113


RESULT 7
HV61_MOUSE
ID   HV61_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18532;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR   PIR; JT0508; HVMS1B.
DR   PDB; 1KCS; 11-MAY-02.
DR   PDB; 1KCV; 11-MAY-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION 1B43.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13158 MW;  1CB547253681FF74 CRC64;

  Query Match             55.1%;  Score 338.5;  DB 1;  Length 116;
  Best Local Similarity   70.2%;  Pred. No. 4.8e-28;
  Matches   66;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||| |||||||:|||||||:| || | || | |:|| ||  |||:| |::|||| |||||
Db         24 ESGPDLVKPSQSLSLTCTVTGYSITS-GYSWHWIRQFPGNKLEWMGYIHYSGNTSYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
              |||:::  ||||| | |:| |||  ||| |||||
Db         83 KSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR 116


RESULT 8
HV62_MOUSE
ID   HV62_MOUSE     STANDARD;      PRT;   117 AA.
AC   P18533;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 733 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; JT0510; HVMS73.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    117       IG HEAVY CHAIN V REGION 733.
FT   DOMAIN       19   >117       IG-LIKE.
FT   DISULFID     40    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13223 MW;  1595517827F976BE CRC64;

  Query Match             54.6%;  Score 335;  DB 1;  Length 117;
  Best Local Similarity   67.0%;  Pred. No. 1.1e-27;
  Matches   63;  Conservative   11;  Mismatches   20;  Indels    0;  Gaps    0;
```

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||||:::|||||:| || :| | |||:|| ||  ||||| ||:|  | ||||
Db         24 ESGPGLVKPSQSIALTCTVTGISITTGNYRWSWIRQFPGNKLEWIGYIYYSAITSYNPSP 83

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
              ||| |:: ||||| | | : |:|| ||| |||||
Db         84 KSRTTITRDTSKNQFFLEMNSLTAEDTATYYCAR 117


RESULT 9
HV60_MOUSE
ID   HV60_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18531;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region M315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
DR   PIR; JT0509; HVMS31.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN         19    116       IG HEAVY CHAIN V REGION M315.
FT   DOMAIN        19    48        FRAMEWORK-1.
FT   DOMAIN        49    53        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        54    67        FRAMEWORK-2.
FT   DOMAIN        68    84        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        85    116       FRAMEWORK-3.
FT   DISULFID      40    114       BY SIMILARITY.
FT   NON_TER      116    116
SQ   SEQUENCE   116 AA;  13095 MW;  4562E03E53DC9E10 CRC64;

  Query Match             54.2%;  Score 332.5;  DB 1;  Length 116;
  Best Local Similarity   67.0%;  Pred. No. 2e-27;
  Matches   63;  Conservative   13;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||:|:| || | ||||:|:|| ||  |||:| | : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYISYDGSNNYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
              |:||::: ||||| | |:| |||  ||| |||||
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116


RESULT 10
HV02_XENLA
ID   HV02_XENLA     STANDARD;      PRT;   135 AA.
AC   P20957;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region XIG14 precursor (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03632; AAA49791.1; -.
DR   PIR; B31933; B31933.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN         19    135       IG HEAVY CHAIN V REGION XIG14.
FT   DOMAIN        20    128       IG-LIKE.
FT   NON_TER      135    135
SQ   SEQUENCE   135 AA;  15080 MW;  EBC467105C00732E CRC64;

  Query Match             52.9%;  Score 325;  DB 1;  Length 135;
  Best Local Similarity   54.8%;  Pred. No. 1.4e-26;
  Matches   63;  Conservative   17;  Mismatches   31;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||| ||||::| |||||||  : |  |:  |:|||||||||||| |   |:|    ||
Db         23 ESGPGTVKPSESLRLTCTVSGFELSS--YHMHWIRQPPGKGLEWIGVIATGGSTAIADSL 80

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGYTLDNWGQGTLVTVSS 114
              |:|:|:: |  |     |::  :   |||:|||||  : ||  | |||||:|||:|
Db         81 KNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCAREYASGYNFDYWGQGTMVTVTS 135


RESULT 11
HV2B_HUMAN
ID   HV2B_HUMAN     STANDARD;      PRT;   120 AA.
AC   P01815;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region COR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02089; G1HUCO.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
```

```
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    110       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     94
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .).
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13226 MW;  158A8B29AE7EEB98 CRC64;

  Query Match             51.1%;  Score 314;  DB 1;  Length 120;
  Best Local Similarity   55.5%;  Pred. No. 1.7e-25;
  Matches   66;  Conservative   14;  Mismatches   29;  Indels   10;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||| ||||:|||:|||| || |: | |    |:||||||||||:  |    : ||| ||
Db          6 ESGPALVKPTQTLTLTCTFSGFSLSSTGMCVGWIRQPPGKGLEWLARIDWDDDKYYNTSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR------SDGYTLDNWGQGTLVTVSS 114
              ::|:|:| |||:|   | :  |   ||| |||||        || :| ||:|| |||||
Db         66 ETRLTISKDTSRNQVVLTMDPV---DTATYYCARITVIPAPAGY-MDVWGRGTPVTVSS 120


RESULT 12
HV2C_HUMAN
ID   HV2C_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01816;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region DAW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC       SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02091; G1HUDW.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    113       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13045 MW;  4E13E00214BAD789 CRC64;

  Query Match             48.1%;  Score 295.5;  DB 1;  Length 119;
  Best Local Similarity   52.6%;  Pred. No. 1.3e-23;
  Matches   60;  Conservative   16;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||| ||:|:|||:|||| || |:       :|:|||||: |||:     : : ||  ||
Db          6 ESGPALVRPTQTLTLTCTFSGFSLSGETMCVAWIRQPPGEALEWLAWDILNDDKYYGASL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-YTLDNWGQGTLVTVSS 114
              ::|: :| |||||    | : :|   ||| |||||| |    | |||| ||||||
Db         66 ETRLAVSKDTSKNQVVLSMNTVGPGDTATYYCARSCGSQYFDYWGQGILVTVSS 119


RESULT 13
HV2H_HUMAN
ID   HV2H_HUMAN     STANDARD;      PRT;   147 AA.
AC   P04438;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region SESS precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84298107; PubMed=6089186;
RA   Takahashi N., Noma T., Honjo T.;
RT   "Rearranged immunoglobulin heavy chain variable region (VH)
RT   pseudogene that deletes the second complementarity-determining
RT   region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR   PIR; A02090; G2HUCS.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-II REGION SESS.
FT   DOMAIN       20    118       V SEGMENT.
FT   DOMAIN      119    132       D SEGMENT.
FT   DOMAIN      133    147       J SEGMENT.
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  16323 MW;  FCBCDB3D00FB6666 CRC64;

  Query Match             47.9%;  Score 294;  DB 1;  Length 147;
  Best Local Similarity   49.6%;  Pred. No. 2.4e-23;
  Matches   58;  Conservative   15;  Mismatches   34;  Indels   10;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||| ||| : ||:|||| || |: : |   ||:|||||| |||:  |    : ||  ||
Db         25 ESGPALVKATHTLTLTCTFSGLSVNTRGMSVSWIRQPPGKALEWLARIDWDDDKYYGTSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----------GYTLDNWGQGT 108
              ::|:|:| |||||    |::|::  |||| |||||               | |||||
Db         85 ETRLTISKDTSKNQVVLKVTNMDPADTATYYCARMQVTMVREVMITSNAFDIWGQGT 141


RESULT 14
HV01_XENLA
ID   HV01_XENLA     STANDARD;      PRT;   136 AA.
AC   P20956;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region XIG8 precursor (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20484; AAA49774.1; ALT_TERM.
DR   PIR; A31933; A31933.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN         19    136       IG HEAVY CHAIN V REGION XIG8.
FT   DOMAIN        19    128       IG-LIKE.
FT   NON_TER      136    136
SQ   SEQUENCE   136 AA;  15123 MW;  3141838981441963 CRC64;

  Query Match             47.0%;  Score 288.5;  DB 1;  Length 136;
  Best Local Similarity   50.4%;  Pred. No. 8e-23;
  Matches   59;  Conservative   19;  Mismatches   32;  Indels    7;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||  ||||::| |||||||  : |  ||  |:|||| | ||||| :   |:|    ||
Db         23 ESGPGTVKPSESLRLTCTVSGFELTS--YYVYWIRQPPRKTLEWIGVVRTDGSTAIADSL 80

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYC----ARSDGYTLDNWGQGTLVTVSS 114
              |:|:|:: |  |    |::  :   |||:|||    | : ||  ::|||||:|||:|
Db         81 KNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCTSTLAGTAGY-FEHWGQGTMVTVTS 136


RESULT 15
HV44_MOUSE
ID   HV44_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01820;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region PJ14 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00767; CAA24148.1; -.
DR   PIR; A02095; HVMS14.
DR   PDB; 1A7N; 29-APR-98.
DR   PDB; 1A7O; 29-APR-98.
DR   PDB; 1A7P; 29-APR-98.
DR   PDB; 1A7R; 29-APR-98.
DR   PDB; 1G7H; 17-JAN-01.
DR   PDB; 1G7I; 17-JAN-01.
DR   PDB; 1G7J; 17-JAN-01.
DR   PDB; 1G7M; 17-JAN-01.
DR   PDB; 43C9; 24-JUL-02.
DR   PDB; 43CA; 24-JUL-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    115       IG HEAVY CHAIN V REGION PJ14.
FT   DOMAIN       20   >115       IG-LIKE.
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12447 MW;  7569DD4A4843D500 CRC64;

  Query Match             46.9%;  Score 288;  DB 1;  Length 115;
  Best Local Similarity   60.2%;  Pred. No. 7.5e-23;
  Matches   56;  Conservative   15;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||| |||:||:|||||| |:   ||  :||||||||||||:| |:  |:| || :|
Db         25 ESGPGLVAPSQSLSITCTVSGFSLT--GYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSAL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA 94
              |||:::| | ||:   |:: |:   ||| ||||
Db         83 KSRLSISKDNSKSQVFLKMNSLQTDDTARYYCA 115


Search completed: August  8, 2004, 12:14:31
Job time : 6.21818 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 31.2636 Seconds
(without alignments)
1150.508 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	476.5	77.6	492	4	Q7Z374	Q7z374 homo sapien
2	470	76.5	478	4	Q7Z379	Q7z379 homo sapien
3	466	75.9	150	4	O95973	O95973 homo sapien
4	466	75.9	496	4	Q96KX8	Q96kx8 homo sapien
5	463.5	75.5	119	4	Q9UL73	Q9ul73 homo sapien
6	457	74.4	613	4	Q96EY0	Q96ey0 homo sapien
7	429	69.9	130	4	Q8IZD7	Q8izd7 homo sapien
8	427	69.5	139	4	Q86SX2	Q86sx2 homo sapien
9	426.5	69.5	588	4	Q8WUX4	Q8wux4 homo sapien
10	426.5	69.5	597	4	Q9BU10	Q9bu10 homo sapien
11	426.5	69.5	618	4	Q96AA6	Q96aa6 homo sapien
12	422.5	68.8	597	4	Q9BQB8	Q9bqb8 homo sapien
13	413	67.3	473	4	Q8TC63	Q8tc63 homo sapien
14	386	62.9	116	4	Q7Z3Y6	Q7z3y6 homo sapien
15	382.5	62.3	479	11	Q99M22	Q99m22 mus musculu
16	365	59.4	122	4	Q9UL75	Q9ul75 homo sapien
17	346.5	56.4	121	4	Q9UL96	Q9ul96 homo sapien
18	341	55.5	118	11	Q811U5	Q811u5 mus musculu
19	339	55.2	121	11	Q99NG4	Q99ng4 mus musculu
20	335	54.6	482	11	Q91X92	Q91x92 mus musculu
21	315.5	51.4	118	4	Q9UL74	Q9ul74 homo sapien
22	297.5	48.5	493	4	Q8NCL6	Q8ncl6 homo sapien
23	294	47.9	613	4	Q8WUK1	Q8wuk1 homo sapien
24	293.5	47.8	116	4	Q9UL93	Q9ul93 homo sapien
25	292.5	47.6	597	4	Q96BB9	Q96bb9 homo sapien
26	291	47.4	147	4	Q9Y509	Q9y509 homo sapien
27	290	47.2	484	11	Q8VEA0	Q8vea0 mus musculu
28	289	47.1	118	4	Q9UL72	Q9ul72 homo sapien
29	286.5	46.7	113	4	Q9UL90	Q9ul90 homo sapien
30	282	45.9	145	11	Q924P7	Q924p7 mus musculu
31	282	45.9	145	11	Q924R1	Q924r1 mus musculu
32	281	45.8	145	11	Q924R4	Q924r4 mus musculu
33	279.5	45.5	117	11	Q9QXE9	Q9qxe9 mus musculu
34	279.5	45.5	121	4	Q9UL71	Q9ul71 homo sapien
35	279.5	45.5	481	11	Q91WT1	Q91wt1 mus musculu
36	279.5	45.5	486	11	Q91Z07	Q91z07 mus musculu
37	279.5	45.5	499	4	Q8N5K4	Q8n5k4 homo sapien
38	279	45.4	494	4	Q96K68	Q96k68 homo sapien
39	278.5	45.4	142	11	Q924Q1	Q924q1 mus musculu
40	278	45.3	298	11	Q9QYF0	Q9qyf0 mus musculu
41	277	45.1	118	4	Q9UL91	Q9ul91 homo sapien
42	276.5	45.0	117	11	Q9QXF0	Q9qxf0 mus musculu
43	275.5	44.9	119	5	Q9GYZ2	Q9gyz2 schistosoma
44	275.5	44.9	480	11	Q91XE1	Q91xe1 mus musculu
45	275	44.8	112	4	Q9HCC1	Q9hcc1 homo sapien

ALIGNMENTS

RESULT 1
Q7Z374
ID Q7Z374 PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN DKFZP686C02218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX538077; CAD98001.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 77.6%; Score 476.5; DB 4; Length 492;
Best Local Similarity 76.9%; Pred. No. 2e-41;
Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||: :  ||| |:||||||||||||:||:: ||||:|||
Db         37 ESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTYYSPSL 96

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR----SDGYTLDNWGQGTLVTVSS 114
              |||:|: |||||||||||||||||||||||||| |       |:  | ||||||||||
Db         97 KSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYGW-FDPWGQGTLVTVSS 152
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RESULT 2
Q7Z379

```
ID   Q7Z379      PRELIMINARY;      PRT;   478 AA.
AC   Q7Z379;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686K04218 (Fragment).
GN   DKFZP686K04218.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538066; CAD97996.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   478 AA;  51620 MW;  4AFCB541F3217CA1 CRC64;

  Query Match             76.5%;  Score 470;  DB 4;  Length 478;
  Best Local Similarity   75.7%;  Pred. No. 9.3e-41;
  Matches   87;  Conservative   14;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||||||||||||||| || |:|||:|| ||:||||:| ||:||:|||||||
Db         24 ESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTYYNPSL 83

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGY--TLDNWGQGTLVTVSS 114
              :||:::|:|||| |||| |:||||||:||| |     | ||||:|||||
Db         84 ESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVGLGTAFDIWGQGTVVTVSS 138


RESULT 3
O95973
ID   O95973      PRELIMINARY;      PRT;   150 AA.
AC   O95973;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH4 heavy chain variable region precursor (Fragment).
GN   IGM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT   "Clonal proliferation of IgM secreting B cell in the synovium of
RT   Behcet's patient with arthritis.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF103795; AAC79084.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   >150       VH4 HEAVY CHAIN VARIABLE REGION.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16315 MW;  85664E04938AA7C9 CRC64;

  Query Match             75.9%;  Score 466;  DB 4;  Length 150;
  Best Local Similarity   76.1%;  Pred. No. 5.8e-41;
  Matches   86;  Conservative   12;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:||||:|||||||| |  ||| |:|||| |||||||::::||: ||||||

Db         25 ESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDYYNPSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||:|:||||||| |||||:|||||||||||||     | || ||:|||||
Db         85 KSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTMVTVSS 137


RESULT 4
Q96KX8
ID   Q96KX8      PRELIMINARY;      PRT;   496 AA.
AC   Q96KX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016369; AAH16369.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53391 MW;  D346929849040D69 CRC64;

  Query Match             75.9%;  Score 466;  DB 4;  Length 496;
  Best Local Similarity   74.2%;  Pred. No. 2.6e-40;
  Matches   89;  Conservative   10;  Mismatches   13;  Indels    8;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||| |:|||||||||||||| |  ||| |:|||||||||| | |:|| |||||||
Db         25 ESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITYYNPSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-------LDNWGQGTLVTVSS 114
              |||:|:|||||||  ||:: ||||||||||:|||  ||:       :| ||||||||||
Db         85 KSRVTISVDTSKNQLSLKVRSVTAADTAVYFCAR-HGYSRSGRTGAIDYWGQGTLVTVSS 143


RESULT 5
Q9UL73
ID   Q9UL73      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
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DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13219 MW;  1BDB86B6420EA0BE CRC64;

  Query Match             75.5%;  Score 463.5;  DB 4;  Length 119;
  Best Local Similarity   77.6%;  Pred. No. 7.9e-41;
  Matches   90;  Conservative    9;  Mismatches   12;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||:||||||||||||| ||:||:| | |||
Db          6 ESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYTPSL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG---YTLDNWGQGTLVTVSS 114
              |||:|:||| ||| |||:|||:||||||||:|||       |  | ||||||||||
Db         64 KSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNWGPYYFDYWGQGTLVTVSS 119


RESULT 6
Q96EY0
ID   Q96EY0      PRELIMINARY;      PRT;   613 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67273 MW;  31214203FB8421E7 CRC64;

  Query Match             74.4%;  Score 457;  DB 4;  Length 613;
  Best Local Similarity   78.0%;  Pred. No. 2.9e-39;
  Matches   92;  Conservative    7;  Mismatches   11;  Indels    8;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||:||| |||||||| || ||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDN-----WGQGTLVTVSS 114
              |||:||||||||| |||:|:|||||||||||||| |  : |       ||||||||||
Db         83 KSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCA-SQPWELPTVGLFYWGQGTLVTVSS 139


RESULT 7
Q8IZD7
ID   Q8IZD7      PRELIMINARY;      PRT;   130 AA.
AC   Q8IZD7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-thyroglobulin heavy chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jang Y.-J., Chung J., Park J.-Y.;
RT   "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT   Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145445; AAN64329.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  13901 MW;  036131FC6EC1551E CRC64;

  Query Match             69.9%;  Score 429;  DB 4;  Length 130;
  Best Local Similarity   68.8%;  Pred. No. 3.6e-37;
  Matches   86;  Conservative   12;  Mismatches   15;  Indels   12;  Gaps    4;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNT-----Y 56
              :|||||||||:|||||||||||||| |  ||| |:|| |||||||||::|:||:|     |
Db          6 QSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTYSGSPY 65

Qy         57 YNPSLKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR----SDG--YT-LDNWGQGTL 109
              | |||:||: :|||||||  ||||:|||||||||||||     | |  |    :|||| |
Db         66 YAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFQHWGQGFL 125

Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130


RESULT 8
Q86SX2
ID   Q86SX2      PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)
DE   of Homo sapiens (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;
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  Query Match             69.5%;  Score 427;  DB 4;  Length 139;
  Best Local Similarity   85.1%;  Pred. No. 6.4e-37;
  Matches   80;  Conservative    8;  Mismatches    4;  Indels    2;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||:|||||||||||| ||:||:| |||||
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 95

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
              |||:|:|||||| |||:|:|||||||||||||
Db         96 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129


RESULT 9
Q8WUX4
ID   Q8WUX4      PRELIMINARY;      PRT;   588 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   588 AA;  64438 MW;  FC60DBAD82B39FD7 CRC64;

  Query Match             69.5%;  Score 426.5;  DB 4;  Length 588;
  Best Local Similarity   70.0%;  Pred. No. 4.3e-36;
  Matches   84;  Conservative   10;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||:||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |:|:||||||    ||:|:|| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 10
Q9BU10
ID   Q9BU10      PRELIMINARY;      PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

  Query Match             69.5%;  Score 426.5;  DB 4;  Length 597;
  Best Local Similarity   70.0%;  Pred. No. 4.4e-36;
  Matches   84;  Conservative   10;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||:||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |:|:||||||    ||:|:|| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 11
Q96AA6
ID   Q96AA6      PRELIMINARY;      PRT;   618 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   618 AA;  67758 MW;  96DBD4C7C696E0A6 CRC64;

  Query Match             69.5%;  Score 426.5;  DB 4;  Length 618;
  Best Local Similarity   70.0%;  Pred. No. 4.6e-36;
  Matches   84;  Conservative   10;  Mismatches   15;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||:||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |:|:||||||    ||:|:|| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 12
Q9BQB8
ID   Q9BQB8      PRELIMINARY;      PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle, and Lymph;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;

  Query Match             68.8%;  Score 422.5;  DB 4;  Length 597;
  Best Local Similarity   70.0%;  Pred. No. 1.2e-35;
  Matches   84;  Conservative    9;  Mismatches   16;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||:||||||||||||| | ||| | |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGITNYNPSLKS 84

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |:|:||||||   ||:|:|| ||||||||||         :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 13
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   GO; GO:0005507; F:copper ion binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match             67.3%;  Score 413;  DB 4;  Length 473;
  Best Local Similarity   69.0%;  Pred. No. 8.6e-35;
  Matches   80;  Conservative   11;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||:||| |||||||||| |: |  ||| |||||||||||||| |  ||| ||:|||
Db         32 ESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQPPGKGLEWIGTINFSGNMYYSPSL 91

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTL----DNWGQGTLVTVS 113
              :||:||| | |:| | |:| ||||||||||||||   |: :     :|||| ||:||
Db         92 RSRVTMSADMSENSFYLKLDSVTAADTAVYYCAA--GHLVMGFGAHWGQGKLVSVS 145


RESULT 14
Q7Z3Y6
ID   Q7Z3Y6      PRELIMINARY;      PRT;   116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   VH4-34.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RT   "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT   indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT   cell precursor in a germinal center.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
FT   NON_TER       1       1
FT   NON_TER     116     116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A846616C908 CRC64;

  Query Match             62.9%;  Score 386;  DB 4;  Length 116;
  Best Local Similarity   65.8%;  Pred. No. 1e-32;
  Matches   73;  Conservative   12;  Mismatches   14;  Indels   12;  Gaps    2;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLKS 63
              | ||:|||:||||:| | |||    ||||:|:|||||||||||| | |||:| |||||||
Db          8 GAGLLKPSETLSLSCAVYGGSF--SGYYWNWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 65

Qy         64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----------GYTLDNW 104
              |:|:|||||||  ||:|:|||||||||||||| :           | :| |
Db         66 RVTISVDTSKNQLSLKLSSVTAADTAVYYCARGEIVVVPAASYYYYYMDVW 116


RESULT 15
Q99M22
ID   Q99M22      PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
```

```
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768E39A138918892 CRC64;

  Query Match             62.3%;  Score 382.5;  DB 11;  Length 479;
  Best Local Similarity   66.7%;  Pred. No. 1.4e-31;
  Matches   76;  Conservative   15;  Mismatches   20;  Indels    3;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||:|:| || | ||||:|:|| ||  |||:| | : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYINYDGSNNYNPSL 82

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGTLVTVSS 114
              |:||::: ||||| | |:| |||  ||| |||| | ||:   ||||||||||:
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCA-SRGYSWFPNWGQGTLVTVSA 135


Search completed: August  8, 2004, 12:17:44
Job time : 31.2636 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	614	100.0	114	5	ABG30446	Abg30446 Human IgE
2	608	99.0	114	5	ABG30447	Abg30447 Human IgE
3	546	88.9	114	5	ABG30445	Abg30445 Human IgE
4	507	82.6	473	4	AAB36206	Aab36206 Human imm
5	504.5	82.2	117	7	ADC99784	Adc99784 Anti-huma
6	504.5	82.2	117	7	ADD05388	Add05388 Anti-MUC1
7	502.5	81.8	123	2	AAW78433	Aaw78433 Antibody
8	502.5	81.8	123	5	ABB97976	Abb97976 Heavy cha
9	501	81.6	252	5	ABP45318	Abp45318 Human BLy
10	500.5	81.5	127	4	AAG80217	Aag80217 Human aut
11	500	81.4	126	3	AAB30584	Aab30584 A human v
12	500	81.4	126	5	ABP54970	Abp54970 Anti-idio
13	500	81.4	251	5	ABG80712	Abg80712 Amyloid p
14	500	81.4	254	5	ABG80713	Abg80713 Amyloid p
15	500	81.4	263	5	ABG80714	Abg80714 Human IgG
16	499.5	81.4	120	4	AAB62775	Aab62775 Human HIV
17	498	81.1	123	4	AAB62745	Aab62745 Human HIV
18	496.5	80.9	122	4	AAB62765	Aab62765 Human HIV
19	496	80.8	246	3	AAY15126	Aay15126 Anti-muri
20	495	80.6	118	2	AAY06385	Aay06385 Humanised
21	494.5	80.5	251	6	ABJ19829	Abj19829 Human VEG
22	494	80.5	172	3	AAY93713	Aay93713 The heavy
23	494	80.5	172	6	AAE35892	Aae35892 Human 2.1
24	493.5	80.4	117	7	ADC99776	Adc99776 Anti-huma
25	493.5	80.4	117	7	ADD05380	Add05380 Anti-MUC1
26	493.5	80.4	123	6	ADA89258	Ada89258 Human ant
27	493	80.3	120	6	ADA89198	Ada89198 Human ant
28	493	80.3	252	5	ABP45983	Abp45983 Human BLy
29	492.5	80.2	251	5	ABP44979	Abp44979 Human BLy
30	492.5	80.2	253	5	ABP45608	Abp45608 Human BLy
31	490.5	79.9	117	3	AAY44615	Aay44615 Human ant
32	490.5	79.9	580	6	AAO30915	Aao30915 dI-NHS76
33	490.5	79.9	580	6	AAO30913	Aao30913 dI-NHS76
34	488.5	79.6	119	2	AAW27554	Aaw27554 Human Ab
35	488.5	79.6	119	6	ABJ18676	Abj18676 Antibody
36	488	79.5	118	2	AAY06383	Aay06383 Humanised
37	488	79.5	139	3	AAY56713	Aay56713 Amino aci
38	487.5	79.4	119	7	ADC99796	Adc99796 Anti-huma
39	487.5	79.4	119	7	ADD05400	Add05400 Anti-MUC1
40	487	79.3	130	5	AAU81273	Aau81273 Human trk
41	487	79.3	254	5	ABP45567	Abp45567 Human BLy
42	487	79.3	256	5	ABP45596	Abp45596 Human BLy
43	484	78.8	117	4	AAU02540	Aau02540 Anti-adip
44	484	78.8	122	2	AAR30145	Aar30145 MAb 1-3-1
45	483.5	78.7	129	5	AAU81275	Aau81275 Human trk

ALIGNMENTS

RESULT 1
ABG30446
ID ABG30446 standard; protein; 114 AA.
XX
AC ABG30446;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89638.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 37; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 614; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.4e-45;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 2
ABG30447
ID ABG30447 standard; protein; 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89639.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 38; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 100 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 99.0%; Score 608; DB 5; Length 114;
Best Local Similarity 97.4%; Pred. No. 2.4e-44;
Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||:|||||||||||||:||||||||||||||||||||||||||||||
Db         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 3
ABG30445
ID ABG30445 standard; protein; 114 AA.
XX
AC ABG30445;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 94 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"

FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89637.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 36; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 88.9%; Score 546; DB 5; Length 114;
Best Local Similarity 89.5%; Pred. No. 4.6e-39;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              |||||||||||:|||||:| |||||||||||||||:|| ||||||||| ||||||||||||
Db          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||| ||||||:| ||||| |||||||||||||| |||||| ||||||||||
Db         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
```

RESULT 4
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-4.
XX
KW Human; immune system associated protein; HISAP-4; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR N-PSDB; AAC66522.
XX
PT New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
PS Claim 1; Col 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 473 AA;

Query Match 82.6%; Score 507; DB 4; Length 473;
Best Local Similarity 79.8%; Pred. No. 4.3e-35;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||:|||||| |||||| |||||||||:|||||||||||| ||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD------GYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||| |       | :| ||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143
```

RESULT 5
ADC99784
ID ADC99784 standard; protein; 117 AA.
XX
AC ADC99784;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX

PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99786.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 1; SEQ ID NO 13; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 82.2%; Score 504.5; DB 7; Length 117;
Best Local Similarity 84.2%; Pred. No. 1.6e-35;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| |||||:|:|| |||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||  ||:  | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117
```

RESULT 6
ADD05388
ID ADD05388 standard; protein; 117 AA.
XX
AC ADD05388;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR N-PSDB; ADD05390.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 1; SEQ ID NO 13; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 82.2%; Score 504.5; DB 7; Length 117;
Best Local Similarity 84.2%; Pred. No. 1.6e-35;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| |||||:|:|| |||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||  ||:  | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117
```

RESULT 7
AAW78433
ID AAW78433 standard; protein; 123 AA.
XX
AC AAW78433;
XX
DT 11-MAY-1999 (first entry)
XX
DE Antibody heavy chain targeted to obr clone 26.
XX
KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
XX
OS Synthetic.
XX
PN WO9850431-A2.
XX
PD 12-NOV-1998.
XX
PF 30-APR-1998; 98WO-US008762.
XX
PR 02-MAY-1997; 97US-00850058.
PR 24-JUN-1997; 97US-0050661P.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon R, Carter PJ, Merchant AM, Presta LG;
XX
DR WPI; 1999-070091/06.
XX
PT Selective preparation of multispecific antibodies - with heteromultimeric
PT heavy chain and common light chain components, useful for, e.g. in vivo
PT diagnosis of cancer.
XX
PS Example 4; Fig 5; 69pp; English.
XX
CC This sequence represents the heavy chain variable region for an antibody
CC that binds to the obr clone 26 protein. The sequence encoding the chain
CC is generated by a new method for preparing a multispecific Ab comprising
CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP

CC comprises a multimerisation domain (MD) forming an interface positioned
CC to interact with an interface of a MD of the extra PP; and (ii) the first
CC and extra PPs each have a binding domain, which comprises a heavy chain
CC and a light chain, where the variable light chains of the first and extra
CC PPs comprise a common sequence. The method comprises: (a) culturing a
CC host cell comprising nucleic acid encoding the first PP and extra PP, and
CC the variable light chain, such that the nucleic acid is expressed; and
CC (b) recovering the multispecific Ab from the culture. The method prepares
CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins
CC and Ab-immunoadhesin chimeras. The method allows for the enhanced
CC formation of the desired heteromultimer relative to the undesired
CC heteromultimers and homomultimers. The Abs can be used in immunoassays
CC and for the in vitro or in vivo diagnosis of various diseases, such as
CC cancer
XX
SQ Sequence 123 AA;

Query Match 81.8%; Score 502.5; DB 2; Length 123;
Best Local Similarity 80.7%; Pred. No. 2.5e-35;
Matches 96; Conservative 8; Mismatches 10; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              :|||||||||||||||||||||||| ||||||||:|| |||||||| ||:||:||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              ||||:|:|||||| |||:|:|||||||||||||| |         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 8
ABB97976
ID ABB97976 standard; protein; 123 AA.
XX
AC ABB97976;
XX
DT 06-SEP-2002 (first entry)
XX
DE Heavy chain variable region from antibody obr.26.
XX
KW Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
KW antiviral; vaccine; tumour.
XX
OS Synthetic.
XX
PN US2002062010-A1.
XX
PD 23-MAY-2002.
XX
PF 23-MAY-2001; 2001US-00863693.
XX
PR 02-MAY-1997; 97US-0046816P.
PR 30-APR-1998; 98US-00070166.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon WR, Carter PJ, Merchant AM, Presta LG;
XX
DR WPI; 2002-499676/53.
XX
PT New multispecific antibodies having heteromultimeric and common
PT components are useful to direct treatment to a target site such as a
PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
PT treat infectious disease.
XX
PS Example 4; Fig 5; 36pp; English.
XX
CC The invention relates to a new multispecific antibody, comprising at
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1
CC has a multimerisation domain forming an interface positioned to interact
CC with an interface of a multimerisation domain of PP2, and both
CC polypeptides each comprise a binding domain consisting a heavy chain and
CC a variable light chain, where the light chain has a sequence common to
CC both polypeptides. Hetromultimers of the inventions include bispecific
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin
CC chimeras. The activity of antibodies of the invention may be described
CC as, cytostatic, antibacterial and antiviral. The heteromultimer can be
CC used for redirected cytotoxicity, for example to kill tumour cells, as a
CC vaccine adjuvant, for delivering thrombolytic agents to clots, for
CC converting enzyme activated prodrugs at a target site such as a tumour,
CC for treating infectious diseases, for targeting immune complexes to cell
CC surface receptors or for delivering immunotoxins to tumour cells. The
CC current sequence represents the heavy chain variable region from antibody
CC obr.26 used in the construction of bispecific antibodies
XX
SQ Sequence 123 AA;

Query Match 81.8%; Score 502.5; DB 5; Length 123;
Best Local Similarity 80.7%; Pred. No. 2.5e-35;
Matches 96; Conservative 8; Mismatches 10; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              :|||||||||||||||||||||||| ||||||||:|| |||||||| ||:||:||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              ||||:|:|||||| |||:|:|||||||||||||| |         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 9
ABP45318
ID ABP45318 standard; protein; 252 AA.
XX
AC ABP45318;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1329.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1989-1990; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell

```
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 252 AA;

  Query Match             81.6%;  Score 501;  DB 5;  Length 252;
  Best Local Similarity   78.5%;  Pred. No. 7.1e-35;
  Matches   95;  Conservative   10;  Mismatches    8;  Indels    8;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||:|||||||||||||| |  ||| |:|||||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTL---DNWGQGTLVTVS 113
              |||:|:|||||||  |||:|:|||||||||||||| |     || |   | ||:|||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGDYDILTGYPLHAFDIWGKGTLVTVS 125

Qy        114 S 114
              |
Db        126 S 126


RESULT 10
AAG80217
ID   AAG80217 standard; protein; 127 AA.
XX
AC   AAG80217;
XX
DT   22-JAN-2002  (first entry)
XX
DE   Human autoantibody MICA-6 variable region light chain.
XX
KW   Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;
KW   glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
KW   polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
KW   variable region; light chain; MICA-6.
XX
OS   Homo sapiens.
XX
PN   EP1149914-A2.
XX
PD   31-OCT-2001.
XX
PF   29-MAR-2001; 2001EP-00107702.
XX
PR   10-APR-2000; 2000DE-01017782.
PR   25-MAY-2000; 2000DE-01025840.
XX
PA   (LABO-) LABOR KOCH MERK GMBH.
XX
PI   Richter W,  Rickert M,  Rapp I,  Dangel W;
XX
DR   WPI; 2001-640702/74.
DR   N-PSDB; AAI68766.
XX
PT   New fusion protein, useful for diagnosis of diabetes type I and other
PT   metabolic diseases, is reactive with autoantibodies against both
PT   glutamate decarboxylase and islet cell antigen.
XX
PS   Disclosure; Page 35-36; 68pp; German.
XX
CC   This invention describes a novel fusion protein (I) that has, at its N-
CC   terminus, one or more epitopes that bind specifically to autoantibodies
CC   (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or
CC   more epitopes that bind specifically to antibodies (Ab) directed against
CC   the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding
CC   it, vectors containing (II) and transformed cells, are useful for
CC   diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,
CC   polyglandular autoimmune syndrome or other autoimmune conditions
CC   associated with AAb against GAD65 or IA2. (I) provides a rapid and simple
CC   diagnosis of high specificity and sensitivity, capable of recognizing
CC   antibodies against both IA2 and GAD65, simultaneously. Unlike known
CC   fusions, where the GAD65 component is at the N-terminus, (I) contains
CC   correctly folded conformational epitopes that can react with most MICA
CC   autoantibodies. This sequence represents the human autoantibody MICA-6
CC   variable region light chain used in the method of the invention
XX
SQ   Sequence 127 AA;

  Query Match             81.5%;  Score 500.5;  DB 4;  Length 127;
  Best Local Similarity   78.0%;  Pred. No. 3.8e-35;
  Matches   96;  Conservative    7;  Mismatches   11;  Indels    9;  Gaps    1;

Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||:|||||||||||||| |  ||| |:||||||||||||:||||| |||| |
Db          5 LESGPGLVKPSETLSLTCTVSGGSISSRNYYWGWIRQPPGKGLEWIGSIYHSGRTYYNLS 64

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS---------DGYTLDNWGQGTLVT 111
              ||||:|:|||||||  |||:|:|||||||||||||          | | || ||||| ||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSYCSAVTCYPDYYGLDIWGQGTTVT 124

Qy        112 VSS 114
              |||
Db        125 VSS 127


RESULT 11
AAB30584
ID   AAB30584 standard; protein; 126 AA.
XX
AC   AAB30584;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A human variable heavy chain region of anti-IgE antibody.
XX
KW   Anti-idiotype antibody; C-epsilon3 region; immunoglobulin E; IgE;
KW   anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;
KW   rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
KW   passive immunisation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          30. .37
FT                   /note= "complementarity determining region 1"
FT   Region          51. .67
FT                   /note= "complementarity determining region 2"
FT   Region          100. .115
FT                   /note= "complementarity determining region 3"
XX
PN   WO200063252-A1.
XX
PD   26-OCT-2000.
XX
PF   12-APR-2000; 2000WO-EP003288.
XX
PR   14-APR-1999;   99GB-00008533.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Kricek F,  Stadler B,  Vogel M;
XX
```

DR WPI; 2000-687161/67.
DR N-PSDB; AAC62336.
XX
PT Novel anti-idiotypic antibody against antibodies which inhibit binding of
PT immunoglobulin E to its high affinity receptor, useful in vaccines for
PT treating diseases such as allergy, rhinitis, atopic dermatitis.
XX
PS Claim 4; Fig 5c; 73pp; English.
XX
CC The present sequence represents a human variable heavy chain region of an
CC anti-idiotype antibody that interferes with the binding of the C-epsilon3
CC region of immunoglobulin (Ig)E to the high affinity receptor for IgE,
CC i.e. and anti-IgE antibody. Such an antibody is referred to as a
CC mimobody. The anti-IgE antibody fragment is used as a vaccine, and as a
CC pharmaceutical for treating IgE-mediated diseases such as allergy, in
CC particular asthma, atopic dermatitis, rhinitis, chronic urticaria and
CC food allergies. It is also used to treat IgE-mediated diseases. It is
CC also used for raising polyclonal or monoclonal antibodies. The polyclonal
CC or monoclonal antibodies obtained are useful for treating IgE-mediated
CC diseases by passive immunisation
XX
SQ Sequence 126 AA;

Query Match 81.4%; Score 500; DB 3; Length 126;
Best Local Similarity 78.7%; Pred. No. 4.2e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||:||||||||||||| ||||||:|:|| ||||||||| ||:||:| ||||
Db          5 LESGPGLVKPSETLSLTCTVSGGSISSGGYYWTWIRQRPGKGLEWIGYIYYSGSTSYNPS 64

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--------YTLDNWGQGTLVTV 112
              ||||:|||||||| ||||||||||||||||||||  |        | :| || || |||
Db         65 LKSRVTMSVDTSKNQFSLRLTSVTAADTAVYYCARERGETGLYYPYYYIDVWGTGTTVTV 124

Qy        113 SS 114
              ||
Db        125 SS 126
```

RESULT 12
ABP54970
ID ABP54970 standard; protein; 126 AA.
XX
AC ABP54970;
XX
DT 14-JAN-2003 (first entry)
XX
DE Anti-idiotypic VH sequence mimicking IgE conformational epitope.
XX
KW Human; IgE; immunoglobulin; antibody; epitope; mimotope;
KW lactic acid bacterium; allergy; vaccine; antiallergic; dermatological;
KW antiinflammatory; anti-idiotype.
XX
OS Homo sapiens.
XX
PN EP1239032-A1.
XX
PD 11-SEP-2002.
XX
PF 02-MAR-2001; 2001EP-00105138.
XX
PR 02-MAR-2001; 2001EP-00105138.
XX
PA (NEST) SOC PROD NESTLE SA.
XX
PI Stadler BM, Vogel M, Germond J, Fritsche R;
XX
DR WPI; 2002-684058/74.
XX
PT New bacterial strain of lactic acid bacterium group, expressing surface
PT polypeptide which contains peptide sequence mimicking at least part of
PT conformational epitope of immunoglobulin E, useful for treating allergy.
XX
PS Claim 4; Page 5; 19pp; English.
XX
CC The present invention relates to recombinant strains of lactic acid
CC bacteria that express surface polypeptides containing peptides
CC (mimotopes) or antibody fragments which mimic at least part of a
CC conformational epitope of an IgE molecule. These are used in food and
CC pharmaceutical compositions, in particular vaccines, for the treatment or
CC prevention of an allergic reaction involving IgE, such as rhinitis,
CC atopic dermatitis and erythema. The mimotope peptides or antibody
CC fragments are obtained by screening random peptide and human Fab antibody
CC phage display libraries with an antibody directed to the Fc part of IgG.
CC The present sequence is the protein sequence of an anti-idiotypic Fab
CC heavy chain variable region (VH) sequence mimicking an IgE conformational
CC epitope
XX
SQ Sequence 126 AA;

Query Match 81.4%; Score 500; DB 5; Length 126;
Best Local Similarity 78.7%; Pred. No. 4.2e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||:||||||||||||| ||||||:|:|| ||||||||| ||:||:| ||||
Db          5 LESGPGLVKPSETLSLTCTVSGGSISSGGYYWTWIRQRPGKGLEWIGYIYYSGSTSYNPS 64

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--------YTLDNWGQGTLVTV 112
              ||||:|||||||| ||||||||||||||||||||  |        | :| || || |||
Db         65 LKSRVTMSVDTSKNQFSLRLTSVTAADTAVYYCARERGETGLYYPYYYIDVWGTGTTVTV 124

Qy        113 SS 114
              ||
Db        125 SS 126
```

RESULT 13
ABG80712
ID ABG80712 standard; peptide; 251 AA.
XX
AC ABG80712;
XX
DT 29-NOV-2002 (first entry)
XX
DE Amyloid peptide containing an attachment site #2.
XX
KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;
KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200256907-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000168.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR WPI; 2002-636514/68.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Claim 38; Page 227; 418pp; English.
XX
CC The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (1) a
CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is a modified
CC antigen for use in the array of the invention. The antigen is modified to
CC posses a cleavage site (enterokinase or factor Xa) and a Cysteine-
CC containing N- or C-terminal linker peptide which serves as the attachment
CC point to a virus like particle or bacterial protein (the scaffold
CC protein)
XX
SQ Sequence 251 AA;

Query Match 81.4%; Score 500; DB 5; Length 251;
Best Local Similarity 78.7%; Pred. No. 8.6e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              |||||||||||:|||||||||||||| ||||||:|:|| |||||||| ||:||:| ||||
Db         20 LESGPGLVKPSETLSLTCTVSGGSISSGGYYWTWIRQRPGKGLEWIGYIYYSGSTSYNPS 79

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--------YTLDNWGQGTLVTV 112
              ||||:|||||||| ||||||||||||||||||||  |        | :| || || |||
Db         80 LKSRVTMSVDTSKNQFSLRLTSVTAADTAVYYCARERGETGLYYPYYYIDVWGTGTTVTV 139

Qy        113 SS 114
              ||
Db        140 SS 141
```

RESULT 14
ABG80713
ID ABG80713 standard; peptide; 254 AA.
XX
AC ABG80713;

XX
DT 29-NOV-2002 (first entry)
XX
DE Amyloid peptide containing an attachment site #3.
XX
KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;
KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200256907-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000168.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR WPI; 2002-636514/68.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Claim 38; Page 227; 418pp; English.
XX
CC The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (1) a
CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,

CC angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is a modified
CC antigen for use in the array of the invention. The antigen is modified to
CC posses a cleavage site (enterokinase or factor Xa) and a Cysteine-
CC containing N- or C-terminal linker peptide which serves as the attachment
CC point to a virus like particle or bacterial protein (the scaffold
CC protein)
XX
SQ Sequence 254 AA;

Query Match 81.4%; Score 500; DB 5; Length 254;
Best Local Similarity 78.7%; Pred. No. 8.8e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

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Db         20 LESGPGLVKPSETLSLTCTVSGGSISSGGYYWTWIRQRPGKGLEWIGYIYYSGSTSYNPS 79

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--------YTLDNWGQGTLVTV 112
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Db         80 LKSRVTMSVDTSKNQFSLRLTSVTAADTAVYYCARERGETGLYYPYYYIDVWGTGTTVTV 139

Qy        113 SS 114
              ||
Db        140 SS 141
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RESULT 15
ABG80714
ID ABG80714 standard; protein; 263 AA.
XX
AC ABG80714;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human IgG/factor Xa cleavage site fusion protein from pCep--Xa-Fc*.
XX
KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;
KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200256907-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000168.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR WPI; 2002-636514/68.
DR N-PSDB; ABS66508.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Example 1; Fig 1; 418pp; English.
XX
CC The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (1) a
CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is a modified
CC antigen for use in the array of the invention. The antigen is modified to
CC posses a cleavage site (enterokinase or factor Xa) and a Cysteine-
CC containing N- or C-terminal linker peptide which serves as the attachment
CC point to a virus like particle or bacterial protein (the scaffold
CC protein)
XX
SQ Sequence 263 AA;

Query Match 81.4%; Score 500; DB 5; Length 263;
Best Local Similarity 78.7%; Pred. No. 9.1e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

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Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||||:|||||||||||||| ||||||:|:|| ||||||||| ||:||:| ||||
Db         20 LESGPGLVKPSETLSLTCTVSGGSISSGGYYWTWIRQRPGKGLEWIGYIYYSGSTSYNPS 79

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--------YTLDNWGQGTLVTV 112
              ||||:|||||||| ||||||||||||||||||||  |        | :| || || |||
Db         80 LKSRVTMSVDTSKNQFSLRLTSVTAADTAVYYCARERGETGLYYPYYYIDVWGTGTTVTV 139

Qy        113 SS 114
              ||
Db        140 SS 141
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Search completed: August 8, 2004, 12:13:46
Job time : 47.8091 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 38.5182 Seconds
(without alignments)
928.389 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	614	100.0	114	14	US-10-027-725A-8	Sequence 8, Appli
2	600	97.7	114	14	US-10-027-725A-9	Sequence 9, Appli
3	546	88.9	114	14	US-10-027-725A-7	Sequence 7, Appli
4	510.5	83.1	121	15	US-10-309-762-152	Sequence 152, App
5	510	83.1	118	15	US-10-309-762-138	Sequence 138, App
6	509.5	83.0	123	15	US-10-309-762-10	Sequence 10, Appl
7	507.5	82.7	125	15	US-10-309-762-11	Sequence 11, Appl
8	507	82.6	120	15	US-10-309-762-13	Sequence 13, Appl
9	507	82.6	120	15	US-10-309-762-144	Sequence 144, App
10	507	82.6	122	15	US-10-309-762-147	Sequence 147, App
11	506	82.4	221	10	US-09-972-656-80	Sequence 80, Appl
12	505.5	82.3	121	15	US-10-309-762-151	Sequence 151, App
13	504.5	82.2	117	14	US-10-330-613-13	Sequence 13, Appl
14	504.5	82.2	117	14	US-10-330-530-13	Sequence 13, Appl
15	504.5	82.2	117	16	US-10-660-357-13	Sequence 13, Appl
16	503.5	82.0	119	15	US-10-309-762-140	Sequence 140, App
17	502.5	81.8	123	15	US-10-309-762-12	Sequence 12, Appl
18	502	81.8	124	15	US-10-309-762-75	Sequence 75, Appl
19	502	81.8	143	15	US-10-309-762-96	Sequence 96, Appl
20	501	81.6	252	10	US-09-880-748-1329	Sequence 1329, Ap
21	501	81.6	252	12	US-10-293-418-1329	Sequence 1329, Ap
22	500	81.4	120	15	US-10-309-762-128	Sequence 128, App
23	500	81.4	120	15	US-10-309-762-139	Sequence 139, App
24	500	81.4	121	12	US-10-453-698-137	Sequence 137, App
25	500	81.4	121	15	US-10-308-817-137	Sequence 137, App
26	500	81.4	126	9	US-09-974-449-6	Sequence 6, Appli
27	499.5	81.4	135	16	US-10-388-214A-34	Sequence 34, Appl
28	499	81.3	116	15	US-10-309-762-127	Sequence 127, App
29	498.5	81.2	125	15	US-10-309-762-8	Sequence 8, Appli
30	498.5	81.2	125	15	US-10-309-762-16	Sequence 16, Appl
31	497.5	81.0	119	15	US-10-309-762-131	Sequence 131, App
32	497	80.9	110	15	US-10-309-762-74	Sequence 74, Appl
33	496.5	80.9	123	15	US-10-309-762-9	Sequence 9, Appli
34	496.5	80.9	127	15	US-10-309-762-14	Sequence 14, Appl
35	495.5	80.7	113	15	US-10-309-762-148	Sequence 148, App
36	495	80.6	118	14	US-10-078-757B-52	Sequence 52, Appl
37	494.5	80.5	125	15	US-10-309-762-153	Sequence 153, App
38	494.5	80.5	251	14	US-10-120-414-75	Sequence 75, Appl
39	494	80.5	172	14	US-10-153-382-21	Sequence 21, Appl
40	493.5	80.4	117	14	US-10-330-613-5	Sequence 5, Appli
41	493.5	80.4	117	14	US-10-330-530-5	Sequence 5, Appli
42	493.5	80.4	117	16	US-10-660-357-5	Sequence 5, Appli
43	493.5	80.4	123	12	US-10-371-942-102	Sequence 102, App
44	493.5	80.4	123	15	US-10-309-762-17	Sequence 17, Appl
45	493	80.3	120	12	US-10-371-942-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match 100.0%; Score 614; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.5e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
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Db         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
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RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:

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;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-9

  Query Match             97.7%;  Score 600;  DB 14;  Length 114;
  Best Local Similarity   96.5%;  Pred. No. 1.4e-47;
  Matches  110;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
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Qy         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
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RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-7

  Query Match             88.9%;  Score 546;  DB 14;  Length 114;
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Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60
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RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-152

  Query Match             83.1%;  Score 510.5;  DB 15;  Length 121;
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  Matches   96;  Conservative    8;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| ||||||||:|| |||||||| ||:|:|||||||
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Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD---GYTLDNWGQGTLVTVSS 114
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RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-138

  Query Match             83.1%;  Score 510;  DB 15;  Length 118;
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              |||||||||||||||||||||||||| ||||||||:|| |||||||| ||:|:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||    |   | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYGSGSDYWGQGTLVTVSS 118


RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
```

```
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-10

  Query Match            83.0%;  Score 509.5;  DB 15;  Length 123;
  Best Local Similarity  82.2%;  Pred. No. 3.2e-39;
  Matches   97;  Conservative    8;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| ||||||||:|| ||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS-----DGYTLDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||||||||:      |  || ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARAGKYYGSGSYLDYWGQGTLVTVSS 123


RESULT 7
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-11

  Query Match            82.7%;  Score 507.5;  DB 15;  Length 125;
  Best Local Similarity  81.7%;  Pred. No. 4.9e-39;
  Matches   98;  Conservative    7;  Mismatches    8;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||:|| ||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGNTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS-----DGY--TLDNWGQGTLVTVSS 114
              |||||:|||||||  |||:|:|||||||||||||:      ||   | |||||:|||||
Db         66 KSRITISVDTSKNQFSLKLSSVTAADTAVYYCARTYYDFLTGYPDAFDIWGQGTMVTVSS 125


RESULT 8
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-13

  Query Match            82.6%;  Score 507;  DB 15;  Length 120;
  Best Local Similarity  83.6%;  Pred. No. 5.2e-39;
  Matches   97;  Conservative    8;  Mismatches    7;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||:|| ||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT---LDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||||||||| |||      | ||:|||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 9
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-144

  Query Match            82.6%;  Score 507;  DB 15;  Length 120;
  Best Local Similarity  83.6%;  Pred. No. 5.2e-39;
  Matches   97;  Conservative    8;  Mismatches    7;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||:|| ||||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT---LDNWGQGTLVTVSS 114
              |||:|:|||||||  |||:|:|||||||||||||| |||      | ||:|||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 10
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
```

```
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-147

  Query Match             82.6%;  Score 507;  DB 15;  Length 122;
  Best Local Similarity   82.1%;  Pred. No. 5.3e-39;
  Matches   96;  Conservative    8;  Mismatches    9;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| ||||||||:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR----SDGYTLDNWGQGTLVTVSS 114
              |||:|:||||||| |||:|:|||||||||||||      || :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYDILTGYGMDVWGQGTTVTVSS 122


RESULT 11
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
;  APPLICANT: Deshpande, Rajendra
;  APPLICANT:  Tsai, Mei-Mei
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: US/09/972,656
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-972-656-80

  Query Match             82.4%;  Score 506;  DB 10;  Length 221;
  Best Local Similarity   83.2%;  Pred. No. 1.2e-38;
  Matches   94;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||| |||||| |||| |||:|||||||||||| |||||:|||||||
Db          6 ESGPGLVKPSETLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIGYIYHSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||:|:||| ||| |||:|:|||||||||||||| |    | ||||||||||
Db         66 KSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARGDWGYFDYWGQGTLVTVSS 118


RESULT 12
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-151

  Query Match             82.3%;  Score 505.5;  DB 15;  Length 121;
  Best Local Similarity   82.8%;  Pred. No. 7.2e-39;
  Matches   96;  Conservative    8;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| ||||||||:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||:|:||||||| |||:|:|||||||||||||      || :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVLLWFGYGMDVWGQGTTVTVSS 121


RESULT 13
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
;  FILE REFERENCE: ABGENIX.022A
;  CURRENT APPLICATION NUMBER: US/10/330,613
;  CURRENT FILING DATE:  2002-12-26
;  PRIOR APPLICATION NUMBER: 60/346299
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-330-613-13

  Query Match             82.2%;  Score 504.5;  DB 14;  Length 117;
  Best Local Similarity   84.2%;  Pred. No. 8.6e-39;
  Matches   96;  Conservative    9;  Mismatches    6;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| ||||||:|:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||  ||:  | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117


RESULT 14
US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
;  FILE REFERENCE: ABGENIX.031A
;  CURRENT APPLICATION NUMBER: US/10/330,530
;  CURRENT FILING DATE:  2002-12-26
;  PRIOR APPLICATION NUMBER: US 60/346414
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
```

```
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-330-530-13

  Query Match             82.2%;  Score 504.5;  DB 14;  Length 117;
  Best Local Similarity   84.2%;  Pred. No. 8.6e-39;
  Matches   96;  Conservative    9;  Mismatches    6;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| ||||||:|:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||  ||:  | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117


RESULT 15
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
;  APPLICANT: Bar-Eli, Menashe
;  APPLICANT:  Green, Larry L.
;  TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
;  TITLE OF INVENTION:  ANTIGEN
;  FILE REFERENCE: ABGENIX.030C1
;  CURRENT APPLICATION NUMBER: US/10/660,357
;  CURRENT FILING DATE:  2003-09-10
;  PRIOR APPLICATION NUMBER: 10/330,580
;  PRIOR FILING DATE: 2002-12-26
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-660-357-13

  Query Match             82.2%;  Score 504.5;  DB 16;  Length 117;
  Best Local Similarity   84.2%;  Pred. No. 8.6e-39;
  Matches   96;  Conservative    9;  Mismatches    6;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| ||||||:|:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||  ||:  | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117


Search completed: August  8, 2004, 12:43:20
Job time : 38.5182 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	507	82.6	473	3	US-09-049-672A-4	Sequence 4, Appli
2	494	80.5	122	1	US-08-360-125-11	Sequence 11, Appl
3	494	80.5	122	2	US-08-450-578-11	Sequence 11, Appl
4	494	80.5	122	2	US-09-017-628-11	Sequence 11, Appl
5	494	80.5	122	2	US-09-014-880-11	Sequence 11, Appl
6	494	80.5	122	4	US-08-450-363-11	Sequence 11, Appl
7	494	80.5	172	4	US-09-472-087-7	Sequence 7, Appli
8	494	80.5	172	4	US-09-472-087-86	Sequence 86, Appl
9	488.5	79.6	119	4	US-09-025-769B-39	Sequence 39, Appl
10	488.5	79.6	119	4	US-09-025-769B-65	Sequence 65, Appl
11	488	79.5	118	4	US-09-025-769B-25	Sequence 25, Appl
12	478	77.9	487	4	US-09-800-729-145	Sequence 145, App
13	473.5	77.1	119	1	US-08-360-125-5	Sequence 5, Appli
14	473.5	77.1	119	2	US-08-450-578-5	Sequence 5, Appli
15	473.5	77.1	119	2	US-09-017-628-5	Sequence 5, Appli
16	473.5	77.1	119	2	US-09-014-880-5	Sequence 5, Appli
17	473.5	77.1	119	4	US-08-450-363-5	Sequence 5, Appli
18	459.5	74.8	142	2	US-08-480-774A-2	Sequence 2, Appli
19	458.5	74.7	250	4	US-10-039-785-50	Sequence 50, Appl
20	458	74.6	244	4	US-08-918-148-79	Sequence 79, Appl
21	453	73.8	118	3	US-08-545-809A-116	Sequence 116, App
22	453	73.8	126	1	US-08-276-852-142	Sequence 142, App
23	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
24	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
25	453	73.8	126	5	PCT-US95-08743-142	Sequence 142, App
26	446.5	72.7	119	2	US-08-652-816A-10	Sequence 10, Appl
27	446	72.6	118	3	US-08-545-809A-123	Sequence 123, App
28	446	72.6	278	3	US-09-260-527-3	Sequence 3, Appli
29	445.5	72.6	123	4	US-08-793-450-4	Sequence 4, Appli
30	445.5	72.6	472	4	US-08-793-450-8	Sequence 8, Appli
31	445	72.5	118	4	US-09-343-698-6	Sequence 6, Appli
32	445	72.5	118	4	US-08-325-955-6	Sequence 6, Appli
33	443	72.1	118	3	US-08-545-809A-142	Sequence 142, App
34	441	71.8	244	4	US-10-039-785-44	Sequence 44, Appl
35	440.5	71.7	124	1	US-08-478-039-78	Sequence 78, Appl
36	440.5	71.7	124	1	US-08-476-349A-78	Sequence 78, Appl
37	439.5	71.6	476	3	US-08-487-550-12	Sequence 12, Appl
38	439.5	71.6	476	4	US-09-526-098-12	Sequence 12, Appl
39	439	71.5	118	2	US-08-652-816A-13	Sequence 13, Appl
40	438	71.3	832	3	US-08-630-820-7	Sequence 7, Appli
41	438	71.3	832	4	US-09-273-453-7	Sequence 7, Appli
42	436.5	71.1	219	4	US-09-460-384-37	Sequence 37, Appl
43	434.5	70.8	123	1	US-08-137-117D-64	Sequence 64, Appl
44	434.5	70.8	123	2	US-08-436-717-64	Sequence 64, Appl
45	434.5	70.8	138	1	US-08-137-117D-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANCTUT01

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;      CLONE:  1513264
US-09-049-672A-4

  Query Match             82.6%;  Score 507;  DB 3;  Length 473;
  Best Local Similarity   79.8%;  Pred. No. 6.8e-43;
  Matches   95;  Conservative    9;  Mismatches    9;  Indels    6;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||:|||||| |||||| ||||||||:|||||||||||| ||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD------GYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||| |       | :| ||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143


RESULT 2
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 5767246ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,125
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human antibody 1-3-1
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

  Query Match             80.5%;  Score 494;  DB 1;  Length 122;
  Best Local Similarity   78.6%;  Pred. No. 2.8e-42;
  Matches   92;  Conservative   10;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||| |:|||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----GYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||||       | :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 3
US-08-450-578-11
; Sequence 11, Application US/08450578
; Patent No. 5837845
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 5837845ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,578
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; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.8e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
||||||||||:|||||||||||||| | ||| |:||||||||||||:||:||:|||||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----GYTLDNWGQGTLVTVSS 114
||||:|:||||||| |||:|:|||||||||||||| | :| ||||| |||||
Db 66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122

RESULT 4
US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.8e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
||||||||||:|||||||||||||| | ||| |:||||||||||||:||:||:|||||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----GYTLDNWGQGTLVTVSS 114
||||:|:||||||| |||:|:|||||||||||||| | :| ||||| |||||
Db 66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122

RESULT 5
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-721-8200
;      TELEFAX:  202-721-8250
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      CELL TYPE:  Hybridoma producing human antibody 1-3-1
US-09-014-880-11

  Query Match             80.5%;  Score 494;  DB 2;  Length 122;
  Best Local Similarity   78.6%;  Pred. No. 2.8e-42;
  Matches   92;  Conservative   10;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||| |:|||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----GYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||        | :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 6
US-08-450-363-11
; Sequence 11, Application US/08450363
; Patent No. 6436434
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 6436434ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,363
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human antibody 1-3-1
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-11

  Query Match             80.5%;  Score 494;  DB 4;  Length 122;
  Best Local Similarity   78.6%;  Pred. No. 2.8e-42;
  Matches   92;  Conservative   10;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||| |:|||||||||||:||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD----GYTLDNWGQGTLVTVSS 114
              |||:|:|||||| |||:|:|||||||||||||        | :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSYGGYYYGMDVWGQGTTVTVSS 122


RESULT 7
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
```

```
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-7

  Query Match            80.5%;  Score 494;  DB 4;  Length 172;
  Best Local Similarity  81.6%;  Pred. No. 4.2e-42;
  Matches   93;  Conservative    8;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLK 62
              |||||||||| |||||||||||| |||:||||:|| |||||||||| ||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              ||:|:||||||| |||:|:|||||||||||||||  |  | :| ||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 8
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-86

  Query Match            80.5%;  Score 494;  DB 4;  Length 172;
  Best Local Similarity  81.6%;  Pred. No. 4.2e-42;
  Matches   93;  Conservative    8;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSLK 62
              |||||||||| |||||||||||| |||:||||:|| |||||||||| ||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              ||:|:||||||| |||:|:|||||||||||||||  |  | :| ||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 9
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-39

  Query Match            79.6%;  Score 488.5;  DB 4;  Length 119;
  Best Local Similarity  81.9%;  Pred. No. 9.6e-42;
  Matches   95;  Conservative    9;  Mismatches    7;  Indels    5;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||:|||||||||||| ||:||:| |||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDG-YTLDNWGQGTLVTVSS 114
              |||:|:||||||| |||:|:|||||||||||||||    || | :| ||||||||||
Db         64 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119


RESULT 10
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
```

```
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10021
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/025,769B
;       FILING DATE:  18-FEB-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95 11 3021.0
;       FILING DATE:  18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)596-9000
;       TELEFAX:  (212)596-9090
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-025-769B-65

  Query Match             79.6%;  Score 488.5;  DB 4;  Length 119;
  Best Local Similarity   81.9%;  Pred. No. 9.6e-42;
  Matches   95;  Conservative    9;  Mismatches    7;  Indels    5;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||:|||||||||||||| |  |||||:||||||||||||| ||:||:| |||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDG-YTLDNWGQGTLVTVSS 114
              |||:|:|||||||| |||:|:|||||||||||||||   || | :| ||||||||||
Db         64 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119


RESULT 11
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  118 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-25

  Query Match             79.5%;  Score 488;  DB 4;  Length 118;
  Best Local Similarity   81.7%;  Pred. No. 1.1e-41;
  Matches   94;  Conservative    7;  Mismatches   10;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||:||||||||||||| |||||:| |||||
Db          6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGEIYHSGSTNYNPSL 63

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA--RSDGYTLDNWGQGTLVTVSS 114
              |||:|:|||||||| |||:|:|||||||||||||  | |   | ||||||||||
Db         64 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGGGGVFDYWGQGTLVTVSS 118


RESULT 12
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 145
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-800-729-145

  Query Match             77.9%;  Score 478;  DB 4;  Length 487;
  Best Local Similarity   75.6%;  Pred. No. 5.7e-40;
  Matches   93;  Conservative   10;  Mismatches   10;  Indels   10;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |||:||||:|| |||||||| | ::| |||||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYISYNGVTYYNPSL 84

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARS-----DGYTL-----DNWGQGTLVT 111
              |||:|:|||||:| |||||:||||||||||||:       ||| |     | |||| |||
Db         85 KSRVTISVDTSQNQFSLRLSSVTAADTAVYYCAKDHRATRDGYQLEYRGFDYWGQGILVT 144

Qy        112 VSS 114
              |||
Db        145 VSS 147


RESULT 13
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
```

; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5

Query Match 77.1%; Score 473.5; DB 1; Length 119;
Best Local Similarity 78.1%; Pred. No. 3e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGTLVTVSS 114
Db 66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTMVTVSS 119

RESULT 14
US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids

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;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:
;     ANTI-SENSE:
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:
;       STRAIN:
;       INDIVIDUAL ISOLATE:
;       DEVELOPMENTAL STAGE:
;       HAPLOTYPE:
;       TISSUE TYPE:
;       CELL TYPE:  Hybridoma producing human
;       CELL TYPE:  antibody GAH
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

  Query Match             77.1%;  Score 473.5;  DB 2;  Length 119;
  Best Local Similarity   78.1%;  Pred. No. 3e-40;
  Matches   89;  Conservative   13;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| | |:||:|:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGTLVTVSS 114
              |||:|:|:|||| |||:|:|:|||||||||||||      | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTMVTVSS 119


RESULT 15
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
;  APPLICANT: HOSOKAWA, Saiko
;  APPLICANT: TAGAWA, Toshiaki
;  APPLICANT: HIRAKAWA, Yoko
;  APPLICANT: ITO, No. 5990287ihiko
;  APPLICANT: NAGAIKE, Kazuhiro
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
;  TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;  FILE REFERENCE: 177/527361KH
;  CURRENT APPLICATION NUMBER: US/09/017,628
;  CURRENT FILING DATE: 1998-02-02
;  EARLIER APPLICATION NUMBER: 08/360,125
;  EARLIER FILING DATE: 1994-12-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

  Query Match             77.1%;  Score 473.5;  DB 2;  Length 119;
  Best Local Similarity   78.1%;  Pred. No. 3e-40;
  Matches   89;  Conservative   13;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
              |||||||||||||||||||||||||| | |:||:|:|| |||||||| ||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGTLVTVSS 114
              |||:|:|:|||| |||:|:|:|||||||||||||      | |||||:|||||
Db         66 KSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTMVTVSS 119


Search completed: August  8, 2004, 12:20:24
Job time : 14.6455 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 10.0182 Seconds
(without alignments)
1094.593 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	501.5	81.7	135	2	S78051	Ig heavy chain pre
2	497.5	81.0	147	2	S13519	Ig heavy chain V r
3	492.5	80.2	140	2	I37782	Ig variable region
4	490	79.8	130	2	S30534	Ig heavy chain V r
5	488.5	79.6	116	2	S37456	Ig mu chain - huma
6	487.5	79.4	130	2	S31690	Ig heavy chain V r
7	480.5	78.3	121	2	S44113	Ig heavy chain V r
8	479.5	78.1	155	2	S31511	Ig heavy chain - h
9	477.5	77.8	146	2	S09710	Ig heavy chain V r
10	477.5	77.8	155	2	S31512	Ig heavy chain - h
11	473.5	77.1	146	2	S09711	Ig heavy chain V r
12	472.5	77.0	127	2	S19668	Ig heavy chain V r
13	472.5	77.0	128	2	S31514	Ig heavy chain - h
14	472	76.9	137	2	S31676	Ig heavy chain V r
15	469	76.4	99	2	S26803	Ig heavy chain V r
16	467.5	76.1	123	2	S30530	Ig heavy chain V r
17	467	76.1	99	2	S26801	Ig heavy chain V r
18	467	76.1	122	2	S69912	Ig V-D-J region (N
19	465	75.7	139	2	S31586	Ig heavy chain V r
20	464	75.6	99	2	S26802	Ig heavy chain V r
21	461	75.1	145	2	S78055	Ig heavy chain pre
22	460.5	75.0	109	2	PH1673	Ig heavy chain V r
23	459	74.8	110	2	S44110	Ig heavy chain V-D
24	458	74.6	139	2	A41287	Ig heavy chain pre
25	457	74.4	118	2	A26340	Ig heavy chain pre
26	454	73.9	97	2	PL0118	Ig heavy chain V-I
27	454	73.9	99	2	S26899	Ig heavy chain V r
28	452	73.6	135	2	S31604	Ig heavy chain V r
29	451	73.5	118	2	S20780	Ig heavy chain V r
30	451	73.5	129	2	S44114	Ig heavy chain V r
31	448	73.0	99	2	S12418	Ig heavy chain V r
32	447.5	72.9	139	2	S31696	Ig heavy chain V r
33	445.5	72.6	137	2	S31585	Ig heavy chain V r
34	445.5	72.6	140	2	A49045	Ig heavy chain V r
35	445	72.5	120	2	PT0370	Ig mu chain precur
36	444	72.3	126	2	S47010	Ig heavy chain V4.
37	443	72.1	99	2	S26800	Ig heavy chain V r
38	442	72.0	99	2	S12412	Ig heavy chain V r
39	442	72.0	105	2	S44125	Ig lambda chain V
40	442	72.0	118	2	S24443	Ig heavy chain V r
41	442	72.0	140	2	S78052	Ig heavy chain pre
42	441.5	71.9	98	2	S12421	Ig heavy chain V r
43	441.5	71.9	132	2	A38911	Ig heavy chain V r
44	441.5	71.9	140	2	A24770	hypothetical hybri
45	441	71.8	97	2	S26906	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S78051
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78051; S23716
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Molecule type: mRNA
A;Residues: 1-135 <HAR>
A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23716
A;Molecule type: mRNA
A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 501.5; DB 2; Length 135;
Best Local Similarity 82.2%; Pred. No. 2.4e-38;
Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||||||||||  | :|| |||||||||||||| ||:||||:||||
Db         18 ESGPGLVKPSETLSLTCTVSGGSISRGSHYWGWIRQPPGKGLEWIGSIYYSGNTYFNPSL 77

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDGYTLDN---WGQGTLVTVSS 114
              |||||:||||||| |||:||||||||||||||   | ||||    ||||| |||||
Db         78 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGTTVTVSS 135
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RESULT 2
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

  Query Match             81.0%;  Score 497.5;  DB 2;  Length 147;
  Best Local Similarity   82.8%;  Pred. No. 6.1e-38;
  Matches   96;  Conservative    5;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||| |||||||||||||| ||:||:|||||||
Db         32 ESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSL 91

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||     |   | ||||||||||
Db         92 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPLLWFGELFDYWGQGTLVTVSS 147


RESULT 3
I37782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

  Query Match             80.2%;  Score 492.5;  DB 2;  Length 140;
  Best Local Similarity   82.2%;  Pred. No. 1.6e-37;
  Matches   97;  Conservative    6;  Mismatches    8;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||||||||||||||||||||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||| :     |   | ||||||||||
Db         83 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTLVTVSS 140


RESULT 4
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             79.8%;  Score 490;  DB 2;  Length 130;
  Best Local Similarity   78.4%;  Pred. No. 2.5e-37;
  Matches   98;  Conservative    4;  Mismatches   11;  Indels   12;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||| || |||||||| |||||||| || ||:| |||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG------YT------LDNWGQGTL 109
              |||||:|||||| |||:|||||||||||||||||  |      ||      | |||||:
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIWGQGTM 125

Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130


RESULT 5
S37456
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

  Query Match             79.6%;  Score 488.5;  DB 2;  Length 116;
  Best Local Similarity   81.2%;  Pred. No. 3.1e-37;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    9;  Gaps    2;

Qy          6 GLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKSRV 65
              |||||||||||||||||||| |||||||||| |||||||||||:||:||||||||||||
Db          1 GLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRV 60

Qy         66 TMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT--------LDNWGQGTLVTVSS 114
              |:||||||| |||:|||||||||||||||||  ||:        :| ||:|| |||||
Db         61 TISVDTSKNQFSLKLSSVTAADTAVYYCARG-GYSYGYYYYYYYMDVWGKGTTVTVSS 116


RESULT 6
S31690
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

  Query Match             79.4%;  Score 487.5;  DB 2;  Length 130;
  Best Local Similarity   78.7%;  Pred. No. 4.3e-37;
  Matches   96;  Conservative    5;  Mismatches   10;  Indels   11;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||| |  ||||| ||||||||||||||:||:| |||||
Db         11 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWSRQPPGKGLEWIGYIYYSGSTNYNPSL 68
```

```
Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG---------YTLDNWGQGTLVTV 112
              |||||:|||||||  |||:||||||||||||||||             |   | |||||||||
Db         69 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSSVLLWFGELLYYFDYWGQGTLVTV 128

Qy        113 SS 114
              ||
Db        129 SS 130
```

RESULT 7
S44113
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <HAW>
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match   78.3%; Score 480.5; DB 2; Length 121;
  Best Local Similarity   80.2%; Pred. No. 1.7e-36;
  Matches   93; Conservative   6; Mismatches   14; Indels   3; Gaps   2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||  | |   ||| | ||||||||||||  ||:||:|||||||
Db          6 ESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-SDGY--TLDNWGQGTLVTVSS 114
              |||||:|||||||  |||:|||||||| ||||:| | ||    | | |||||||||
Db         66 KSRVTLSVDTSKNQFSLKLSSVTAADTGVYYCSRLSGGYYSDFDYWSQGTLVTVSS 121
```

RESULT 8
S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Reference number: S31509
A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

  Query Match   78.1%; Score 479.5; DB 2; Length 155;
  Best Local Similarity   77.5%; Pred. No. 2.7e-36;
  Matches   93; Conservative   8; Mismatches   10; Indels   9; Gaps   2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||  |  |||||||||||||||||||::|:  ||| |
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPL 95

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-------YTLDNWGQGTLVTVSS 114
              |||||:|||||||  |||::|||||||||||||||  |       | :| ||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTVTVSS 155
```

RESULT 9
S09710
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S09710
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains c
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09710
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

  Query Match   77.8%; Score 477.5; DB 2; Length 146;
  Best Local Similarity   74.0%; Pred. No. 3.8e-36;
  Matches   91; Conservative   11; Mismatches   10; Indels   11; Gaps   2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:||||||:|||||: ||| || |:|||||||||||| |::||:|||||||
Db         25 ESGPGLVKPSETLSLTCSVSGGSVSSGGLYWGWVRQPPGKGLEWIGSIFYSGSTYYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGY----------TLDNWGQGTLVT 111
              |||||:|||| ||:|||:|||||||||||||| |  ||           :| ||||| ||
Db         85 KSRVTISVDTLKNNFSLKLSSVTAADTAVYYCTR-PGYGDTSVRKRVWNMDLWGQGTTVT 143

Qy        112 VSS 114
              |||
Db        144 VSS 146
```

RESULT 10
S31512
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Reference number: S31509
A;Accession: S31512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

  Query Match   77.8%; Score 477.5; DB 2; Length 155;
  Best Local Similarity   76.7%; Pred. No. 4.1e-36;
  Matches   92; Conservative   9; Mismatches   10; Indels   9; Gaps   2;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||  |  |||||||||||||||||||::|:  ||| :
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSATYNPPI 95

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-------YTLDNWGQGTLVTVSS 114
              |||||:|||||||  |||::|||||||||||||||  |       | :| ||||| |||||
Db         96 KSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYVYYGMDVWGQGTTVTVSS 155
```

RESULT 11
S09711
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

```
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains c
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

  Query Match             77.1%;  Score 473.5;  DB 2;  Length 146;
  Best Local Similarity   73.8%;  Pred. No. 8.8e-36;
  Matches   90;  Conservative   10;  Mismatches   13;  Indels    9;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||:||||||||: | | ||||||||||| |||||||:||:| |||||
Db         25 ESGPGLVKPSETLSVTCTVSGGSVSSSGLYWSWIRQPPGKGPEWIGYIYYSGSTNYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR---------SDGYTLDNWGQGTLVTV 112
              :||||:||||||| |||:| ||||||||||||||           | :| ||:|| |||
Db         85 RSRVTISVDTSKNQFSLKLGSVTAADTAVYYCARVLVSRTSISQYSYYMDVWGKGTTVTV 144

Qy        113 SS 114
              ||
Db        145 SS 146


RESULT 12
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118,'E',120-121,'T',123-126,'F' <JON>
A;Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             77.0%;  Score 472.5;  DB 2;  Length 127;
  Best Local Similarity   74.6%;  Pred. No. 9.4e-36;
  Matches   91;  Conservative    9;  Mismatches   13;  Indels    9;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              :|| ||||||||||||:||| || |||| |||||| |||||||| ::||| |||||||
Db          6 QSGSGLVKPSQTLSLTCSVSGDSISSGGYSWSWIRQPSGKGLEWIGSVHHSGPTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG---------YTLDNWGQGTLVTV 112
              |||||||||||| |||:| ||||||||:|:|||  |          | :| ||:||||||
Db         66 KSRVTMSVDTSKNQFSLKLKSVTAADTAMYFCAREGGSTWRSLYKHYYMDVWGKGTLVTV 125

Qy        113 SS 114
              ||
Db        126 SS 127


RESULT 13
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

  Query Match             77.0%;  Score 472.5;  DB 2;  Length 128;
  Best Local Similarity   78.4%;  Pred. No. 9.4e-36;
  Matches   91;  Conservative    8;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||:|||||||||||||||| |||:|||||| ||  |||| :|| ||:||||| |
Db         13 ESGPGLVRPSQTLSLTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIYFSGSTYYNPFL 72

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR---SDGYTLDNWGQGTLVTVSS 114
              |||| :|||||:| |||||:||| ||||||||||   : ||  | ||||||||||
Db         73 KSRVIISVDTSENQFSLRLTSVTPADTAVYYCARIGYNFGYGFDPWGQGTLVTVSS 128


RESULT 14
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

  Query Match             76.9%;  Score 472;  DB 2;  Length 137;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-35;
  Matches   95;  Conservative    4;  Mismatches   12;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||||||||| |||||||| || ||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              |||||||||||| |||:|||||||||||||||||     | :| ||||| |||||
Db         83 KSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDAPLMYGMDVWGQGTTVTVSS 137


RESULT 15
S26803
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26803
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
```

A;Accession: S26803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WEN>
A;Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 99;
Best Local Similarity 92.6%; Pred. No. 1.5e-35;
Matches 87; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||| || ||||||||||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR 95
              |||||:|||||||  |||:||||||||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 99
```

Search completed: August 8, 2004, 12:18:54
Job time : 10.0182 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 6.21818 Seconds
(without alignments)
954.620 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	439.5	71.6	129	1	HV2F_HUMAN	P01824 homo sapien
2	420	68.4	146	1	HV2I_HUMAN	P06331 homo sapien
3	393.5	64.1	117	1	HV2G_HUMAN	P01825 homo sapien
4	372.5	60.7	137	1	HV46_MOUSE	P01822 mus musculu
5	357.5	58.2	113	1	HV47_MOUSE	P01823 mus musculu
6	349.5	56.9	144	1	HV43_MOUSE	P01819 mus musculu
7	348.5	56.8	116	1	HV61_MOUSE	P18532 mus musculu
8	347	56.5	117	1	HV62_MOUSE	P18533 mus musculu
9	342.5	55.8	116	1	HV60_MOUSE	P18531 mus musculu
10	330	53.7	135	1	HV02_XENLA	P20957 xenopus lae
11	313	51.0	120	1	HV2B_HUMAN	P01815 homo sapien
12	302.5	49.3	119	1	HV2C_HUMAN	P01816 homo sapien
13	293.5	47.8	136	1	HV01_XENLA	P20956 xenopus lae
14	291	47.4	122	1	HV3A_HUMAN	P01762 homo sapien
15	289.5	47.1	125	1	HV2D_HUMAN	P01817 homo sapien
16	289	47.1	114	1	HV3B_HUMAN	P01763 homo sapien
17	288	46.9	115	1	HV44_MOUSE	P01820 mus musculu
18	288	46.9	147	1	HV2H_HUMAN	P04438 homo sapien
19	287.5	46.8	121	1	HV2E_HUMAN	P01818 homo sapien
20	287	46.7	119	1	HV40_MOUSE	P01810 mus musculu
21	286.5	46.7	117	1	HV2B_RABIT	P01828 oryctolagus
22	282	45.9	122	1	HV3G_HUMAN	P01768 homo sapien
23	280	45.6	126	1	HV2A_HUMAN	P01814 homo sapien
24	278	45.3	116	1	HV05_CARAU	P19181 carassius a
25	277.5	45.2	121	1	HV3J_HUMAN	P01771 homo sapien
26	277	45.1	119	1	HV37_MOUSE	P01807 mus musculu
27	276	45.0	116	1	HV45_MOUSE	P01821 mus musculu
28	276	45.0	136	1	HV2C_RABIT	P01829 oryctolagus
29	275	44.8	119	1	HV38_MOUSE	P01808 mus musculu
30	274	44.6	114	1	HV2A_RABIT	P01827 oryctolagus
31	272.5	44.4	117	1	HV41_MOUSE	P01811 mus musculu
32	272.5	44.4	117	1	HV42_MOUSE	P01812 mus musculu
33	272	44.3	122	1	HV3H_HUMAN	P01769 homo sapien
34	271.5	44.2	142	1	HV01_RAT	P01805 rattus norv
35	268	43.6	139	1	HV07_MOUSE	P01751 mus musculu
36	263.5	42.9	115	1	HV3D_HUMAN	P01765 homo sapien
37	263	42.8	118	1	HV51_MOUSE	P06330 mus musculu
38	263	42.8	122	1	HV20_MOUSE	P01789 mus musculu
39	262.5	42.8	117	1	HV12_MOUSE	P01756 mus musculu
40	262	42.7	120	1	HV50_MOUSE	P06329 mus musculu
41	262	42.7	126	1	HV3K_HUMAN	P01772 homo sapien
42	262	42.7	136	1	HV16_MOUSE	P01783 mus musculu
43	261.5	42.6	115	1	HV3F_HUMAN	P01767 homo sapien
44	261.5	42.6	117	1	HV13_MOUSE	P01757 mus musculu
45	258.5	42.1	117	1	HV17_MOUSE	P01786 mus musculu

ALIGNMENTS

RESULT 1
HV2F_HUMAN
ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUWA.
DR HSSP; P01825; 7FAB.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.6%; Score 439.5; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 6.4e-39;
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;

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Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||:|||||| |||| ||  |||| |||||||||||||| :|::|: ||||||
Db          6 ESGPGLVKPSETLSLTCIVSGGPIRRTGYYWGWIRQPPGKGLEWIGGVYYTGSIYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR------------SDGYTLDNWGQGT 108
              : |||:|||||:| ||| | |::|||||:|||||              ||  :| |||||
Db         66 RGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYYDIGTGSDDG--IDVWGQGT 123

Qy        109 LVTVSS 114
               | |||
Db        124 TVHVSS 129
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RESULT 2

```
HV2I_HUMAN
ID   HV2I_HUMAN     STANDARD;      PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146       IG HEAVY CHAIN V-II REGION ARH-77.
FT   DOMAIN       20    117       V SEGMENT.
FT   DOMAIN      118    127       D SEGMENT.
FT   DOMAIN      128    146       J SEGMENT.
FT   DISULFID     42    115       BY SIMILARITY.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16228 MW;  8D7FD52BB218171F CRC64;

  Query Match             68.4%;  Score 420;  DB 1;  Length 146;
  Best Local Similarity   71.1%;  Pred. No. 7.9e-37;
  Matches   86;  Conservative    7;  Mismatches   16;  Indels   12;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||||||:|||||| | |||    ||||||||||||:|||||| | |||:| |  ||||
Db         28 GAGLVKPSETLSLTCAVFGGSF--SGYYWSWIRQPPGRGLEWIGEINHSGSTNYKTSLKS 85

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS---DG-------YTLDNWGQGTLVTVS 113
              |||:|:||||| |||:||||||||||||||||     |       | :| ||||| ||||
Db         86 RVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWNDVDYYYGMDVWGQGTTVTVS 145

Qy        114 S 114
              |
Db        146 S 146


RESULT 3
HV2G_HUMAN
ID   HV2G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01825;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region NEWM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77242302; PubMed=407927;
RA   Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT   "Amino acid sequence of the VH region of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 16:3412-3420(1977).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX   MEDLINE=78066916; PubMed=618887;
RA   Saul F.A., Amzel L.M., Poljak R.J.;
RT   "Preliminary refinement and structural analysis of the Fab fragment
RT   from human immunoglobulin new at 2.0-A resolution.";
RL   J. Biol. Chem. 253:585-597(1978).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90404; G1HUNM.
DR   PDB; 7FAB; 31-JAN-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    111       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   TURN         30     31
FT   STRAND       33     39
FT   TURN         41     42
FT   STRAND       46     51
FT   TURN         53     54
FT   STRAND       57     59
FT   HELIX        61     63
FT   TURN         64     66
FT   STRAND       67     72
FT   TURN         73     76
FT   STRAND       77     82
FT   HELIX        87     89
FT   STRAND       91     98
FT   STRAND      104    107
FT   STRAND      111    115
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12790 MW;  2DA47B509562D237 CRC64;

  Query Match             64.1%;  Score 393.5;  DB 1;  Length 117;
  Best Local Similarity   67.5%;  Pred. No. 3.6e-34;
  Matches   77;  Conservative   16;  Mismatches   18;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              :||||||:|||||||||||| :  :   |::|:|||||:|||||||::: | :    |
Db          6 QSGPGLVRPSQTLSLTCTVSGGSTFSND--YYTWVRQPPGRGLEWIGYVFYHGTSDDTTPL 63

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS-DGYTLDNWGQGTLVTVSS 114
              :||||| |||||| |||||||||||||||||||:     :| ||||:||||||
Db         64 RSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLIAGCIDVWGQGSLVTVSS 117


RESULT 4
HV46_MOUSE
ID   HV46_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=89238351; PubMed=2497341;
RA   Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT   "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT   gene segment.";
RL   Mol. Immunol. 26:431-434(1989).
RN   [2]
RP   SEQUENCE OF 1-31.
RX   MEDLINE=78094475; PubMed=414225;
RA   Jilka R.L., Pestka S.;
RT   "Amino acid sequence of the precursor region of MOPC-315 mouse
RT   immunoglobulin heavy chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN   [3]
RP   SEQUENCE OF 1-21.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [4]
RP   SEQUENCE OF 19-136.
RX   MEDLINE=74170779; PubMed=4524622;
RA   Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT   "Amino-acid sequence of the variable region of the heavy (alpha)
RT   chain of a mouse myeloma protein with anti-hapten activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN   [5]
RP   REVISION TO 53.
RX   MEDLINE=77244979; PubMed=268248;
RA   Hood L., Margolies M.N., Givol D., Zakut R.;
RL   Unpublished results, cited by:
RL   Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL   Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC   -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; M27638; AAA61337.1; -.
DR   EMBL; X07880; CAA30727.1; -.
DR   PIR; PL0102; AVMS35.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     18
FT   CHAIN       19    137       IG HEAVY CHAIN V REGION MOPC 315.
FT   DOMAIN      19     48       FRAMEWORK-1.
FT   DOMAIN      49     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      55     68       FRAMEWORK-2.
FT   DOMAIN      69     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      85    116       FRAMEWORK-3.
FT   DOMAIN     117    126       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     127    137       FRAMEWORK-4.
FT   DISULFID    40    114       BY SIMILARITY.
FT   CONFLICT    15     15       G -> GG (IN REF. 1; CAA30727).
FT   CONFLICT    15     15       G -> H (IN REF. 2).
FT   CONFLICT    77     78       GY -> YG (IN REF. 4).
FT   CONFLICT   102    102       N -> D (IN REF. 4).
FT   CONFLICT   123    123       MISSING (IN REF. 4).
FT   NON_TER    137    137
SQ   SEQUENCE   137 AA;  15399 MW;  FB3828304C2B81DC CRC64;

  Query Match             60.7%;  Score 372.5;  DB 1;  Length 137;
  Best Local Similarity   62.6%;  Pred. No. 6.6e-32;
  Matches   72;  Conservative   18;  Mismatches   22;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||:|||||:|:| || | ||:|:|||| ||  |||:|:| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYFWNWIRQFPGNKLEWLGFIKYDGSNGYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              |:||::: |||:| | |:|:||| ||| |||| :  |  | ||||| :||||
Db         83 KNRVSITRDTSENQFFLKLNSVTTEDTATYYCAGDNDHLYYFDYWGQGTTLTVSS 137


RESULT 5
HV47_MOUSE
ID   HV47_MOUSE     STANDARD;      PRT;   113 AA.
AC   P01823;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-60.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=84024551; PubMed=6414509;
RA   Juszczak E.C., Margolies M.N.;
RT   "Amino acid sequence of the heavy chain variable region from the A/J
RT   mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
RT   idiotype.";
RL   Biochemistry 22:4291-4296(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC       MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC       IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC       STRAIN A/J MICE.
DR   PIR; A02098; G2MS60.
DR   PDB; 1J1O; 18-FEB-03.
DR   PDB; 1J1P; 18-FEB-03.
DR   PDB; 1J1X; 18-FEB-03.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12734 MW;  38DC0E0E3F5075B7 CRC64;

  Query Match             58.2%;  Score 357.5;  DB 1;  Length 113;
  Best Local Similarity   62.8%;  Pred. No. 1.9e-30;
  Matches   71;  Conservative   16;  Mismatches   21;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| ||||||||||||:|:| || |   ||:|||: ||  || :||| :||:|||||||
Db          6 ESGPSLVKPSQTLSLTCSVTGDSITSD--YWNWIRKFPGNKLEHMGYISYSGSTYYNPSL 63

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||:::: ||||| : |:|:|||: ||| |||          ||||||||||:
Db         64 KSRISITRDTSKNQYYLQLNSVTSEDTATYYCT---SLRFAYWGQGTLVTVSA 113


RESULT 6
HV43_MOUSE
ID   HV43_MOUSE     STANDARD;      PRT;   144 AA.
AC   P01819;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOPC 141 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC       DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00768; CAA24149.1; -.
DR   PIR; A02094; G2MS14.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    144       IG HEAVY CHAIN V REGION MOPC 141.
FT   DOMAIN       20    130       IG-LIKE.
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15759 MW;  8E47A7CB3706D30A CRC64;

  Query Match           56.9%;  Score 349.5;  DB 1;  Length 144;
  Best Local Similarity  59.0%;  Pred. No. 1.7e-29;
  Matches   72;  Conservative   18;  Mismatches   21;  Indels   11;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||| |||:||:|||||| |:   ||  :|:|||||||||:| |: :|:| || :|
Db         25 ESGPGLVAPSQSLSITCTVSGFSLT--GYGVNWVRQPPGKGLEWLGTIWGNGSTDYNSTL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCA--------RSDGY-TLDNWGQGTLVTV 112
              |||:|:: | ||:   |:::|:   ||| ||||         ||| | ||| ||||| |||
Db         83 KSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSIYYYGRSDKYFTLDYWGQGTSVTV 142

Qy        113 SS 114
              ||
Db        143 SS 144


RESULT 7
HV61_MOUSE
ID   HV61_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18532;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR   PIR; JT0508; HVMS1B.
DR   PDB; 1KCS; 11-MAY-02.
DR   PDB; 1KCV; 11-MAY-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION 1B43.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13158 MW;  1CB547253681FF74 CRC64;

  Query Match           56.8%;  Score 348.5;  DB 1;  Length 116;
  Best Local Similarity  71.3%;  Pred. No. 1.7e-29;
  Matches   67;  Conservative   11;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| |||||:|||||||:| || | || | |||| ||  |||:|||::|||| |||||
Db         24 ESGPDLVKPSQSLSLTCTVTGYSITS-GYSWHWIRQFPGNKLEWMGYIHYSGNTSYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR 95
              |||:::: ||||| | |:|:|||  ||| |||||
Db         83 KSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR 116


RESULT 8
HV62_MOUSE
ID   HV62_MOUSE     STANDARD;      PRT;   117 AA.
AC   P18533;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 733 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; JT0510; HVMS73.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    117       IG HEAVY CHAIN V REGION 733.
FT   DOMAIN       19   >117       IG-LIKE.
FT   DISULFID     40    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13223 MW;  1595517827F976BE CRC64;

  Query Match           56.5%;  Score 347;  DB 1;  Length 117;
  Best Local Similarity  69.1%;  Pred. No. 2.5e-29;
  Matches   65;  Conservative   11;  Mismatches   18;  Indels    0;  Gaps    0;
```

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||:::|||||:|  || :| | |||||| ||  ||||||||:|  | ||||
Db         24 ESGPGLVKPSQSIALTCTVTGISITTGNYRWSWIRQFPGNKLEWIGYIYYSAITSYNPSP 83

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR 95
              ||| |:: ||||| | | ::|:|| ||| |||||
Db         84 KSRTTITRDTSKNQFFLEMNSLTAEDTATYYCAR 117


RESULT 9
HV60_MOUSE
ID   HV60_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18531;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region M315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
DR   PIR; JT0509; HVMS31.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       IG HEAVY CHAIN V REGION M315.
FT   DOMAIN       19     48       FRAMEWORK-1.
FT   DOMAIN       49     53       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       54     67       FRAMEWORK-2.
FT   DOMAIN       68     84       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       85    116       FRAMEWORK-3.
FT   DISULFID     40    114       BY SIMILARITY.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13095 MW;  4562E03E53DC9E10 CRC64;

  Query Match             55.8%;  Score 342.5;  DB 1;  Length 116;
  Best Local Similarity   68.1%;  Pred. No. 7.3e-29;
  Matches   64;  Conservative   14;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||:|||||:|:| || | ||||:|||| ||  |||:||| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYISYDGSNNYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR 95
              |:|:::: ||||| | |:|:|||  ||| |||||
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116


RESULT 10
HV02_XENLA
ID   HV02_XENLA     STANDARD;      PRT;   135 AA.
AC   P20957;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region XIG14 precursor (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03632; AAA49791.1; -.
DR   PIR; B31933; B31933.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN        19    135       IG HEAVY CHAIN V REGION XIG14.
FT   DOMAIN       20    128       IG-LIKE.
FT   NON_TER     135    135
SQ   SEQUENCE   135 AA;  15080 MW;  EBC467105C00732E CRC64;

  Query Match             53.7%;  Score 330;  DB 1;  Length 135;
  Best Local Similarity   56.5%;  Pred. No. 1.7e-27;
  Matches   65;  Conservative   16;  Mismatches   30;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||| ||||::|  |||||||  : |  |:  |||||||||||||| |   |:|    ||
Db         23 ESGPGTVKPSESLRLTCTVSGFELSS--YHMHWIRQPPGKGLEWIGVIATGGSTAIADSL 80

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDGYTLDNWGQGTLVTVSS 114
              |:|||:: |  |    |::: :   |||:|||||  : ||  | |||||:|||:|
Db         81 KNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCAREYASGYNFDYWGQGTMVTVTS 135


RESULT 11
HV2B_HUMAN
ID   HV2B_HUMAN     STANDARD;      PRT;   120 AA.
AC   P01815;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region COR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02089; G1HUCO.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
```

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DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    110       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     94
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .).
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13226 MW;  158A8B29AE7EEB98 CRC64;

  Query Match             51.0%;  Score 313;  DB 1;  Length 120;
  Best Local Similarity   56.3%;  Pred. No. 9.1e-26;
  Matches   67;  Conservative   13;  Mismatches   29;  Indels   10;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| |||||:|||:|||| || |: | |    |||||||||||:  |    : ||| ||
Db          6 ESGPALVKPTQTLTLTCTFSGFSLSSTGMCVGWIRQPPGKGLEWLARIDWDDDKYYNTSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR------SDGYTLDNWGQGTLVTVSS 114
              ::|:|:| |||:|   | :  |   ||| |||||        || :| ||:|| |||||
Db         66 ETRLTISKDTSRNQVVLTMDPV---DTATYYCARITVIPAPAGY-MDVWGRGTPVTVSS 120


RESULT 12
HV2C_HUMAN
ID   HV2C_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01816;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region DAW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC       SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02091; G1HUDW.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    113       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13045 MW;  4E13E00214BAD789 CRC64;

  Query Match             49.3%;  Score 302.5;  DB 1;  Length 119;
  Best Local Similarity   53.5%;  Pred. No. 1.1e-24;
  Matches   61;  Conservative   17;  Mismatches   35;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| ||:|:|||:|||| || |:       :|||||||: |||: :   : : ||  ||
Db          6 ESGPALVRPTQTLTLTCTFSGFSLSGETMCVAWIRQPPGEALEWLAWDILNDDKYYGASL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-YTLDNWGQGTLVTVSS 114
              ::|: :| |||||   | :::|   ||| |||||| |    | |||| ||||||
Db         66 ETRLAVSKDTSKNQVVLSMNTVGPGDTATYYCARSCGSQYFDYWGQGILVTVSS 119


RESULT 13
HV01_XENLA
ID   HV01_XENLA     STANDARD;      PRT;   136 AA.
AC   P20956;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region XIG8 precursor (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20484; AAA49774.1; ALT_TERM.
DR   PIR; A31933; A31933.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN        19    136       IG HEAVY CHAIN V REGION XIG8.
FT   DOMAIN       19    128       IG-LIKE.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15123 MW;  3141838981441963 CRC64;

  Query Match             47.8%;  Score 293.5;  DB 1;  Length 136;
  Best Local Similarity   52.1%;  Pred. No. 1.1e-23;
  Matches   61;  Conservative   18;  Mismatches   31;  Indels    7;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||| ||||::| |||||||  : |  ||  |||||| | |||||  :   |:|    ||
Db         23 ESGPGTVKPSESLRLTCTVSGFELTS--YYVYWIRQPPRKTLEWIGVVRTDGSTAIADSL 80

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYC----ARSDGYTLDNWGQGTLVTVSS 114
              |:|||:: | |    |::: :   |||:|||    | : ||  ::|||||:|||:|
Db         81 KNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCTSTLAGTAGY-FEHWGQGTMVTVTS 136


RESULT 14
HV3A_HUMAN
ID   HV3A_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01762;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
```

```
DE   Ig heavy chain V-III region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN TRO).
RX   MEDLINE=76023781; PubMed=809331;
RA   Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
RA   Hilschmann N.;
RT   "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
RT   II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT   structure of the complete IgA-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02045; A1HUTR.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    108       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13472 MW;  2E21A11DA04D80F9 CRC64;

  Query Match             47.4%;  Score 291;  DB 1;  Length 122;
  Best Local Similarity   47.5%;  Pred. No. 1.8e-23;
  Matches   57;  Conservative   22;  Mismatches   33;  Indels    8;  Gaps    3;

Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNT-YYNP 59
              ::|| |||||  :| |:|  || | |   :| ||||: |||||:|: ||  ||:| ||
Db          5 VQSGGGLVKPGGSLRLSCVASGFSFRD--FYMSWIRZTPGKGLZWVSYIGGSGSTLYYAD 62

Qy         60 SLKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----YTLDNWGQGTLVTVSS 114
               |:| | |:| | ::    | : |:   :|||||| ::      ::|: ||:| ||||||
Db         63 SVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBFBWSTFSLBYWGZGBLVTVSS 122


RESULT 15
HV2D_HUMAN
ID   HV2D_HUMAN     STANDARD;      PRT;   125 AA.
AC   P01817;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region MCE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81118242; PubMed=6780622;
RA   Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
RA   Litman G.W.;
RT   "Molecular basis for the temperature-dependent insolubility of
RT   cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT   region of McE.";
RL   J. Immunol. 126:1212-1216(1981).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CC       CRYOIMMUNOGLOBULIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02092; MHHUMC.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    113       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13783 MW;  7A1ADF4C40F47BB5 CRC64;

  Query Match             47.1%;  Score 289.5;  DB 1;  Length 125;
  Best Local Similarity   47.5%;  Pred. No. 2.7e-23;
  Matches   57;  Conservative   20;  Mismatches   36;  Indels    7;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||| ||||::||:|||| || |: : |    |||| ||| |||: :|    :  |:|||
Db          6 ESGPTLVKPTETLTLTCTFSGFSLSTSGVGVGWIRQRPGKALEWLAFINWDDDNRYSPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-------LDNWGQGTLVTVSS 114
              :||:| : |||:|   | ::::   |:  |:||    :          | ||||||||||
Db         66 RSRLTGTKDTSRNQVVLTITNMDPVDSGTYFCAHRPPWRFTGNLGGFDXWGQGTLVTVSS 125


Search completed: August  8, 2004, 12:14:31
Job time : 6.21818 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 31.2636 Seconds
(without alignments)
1150.508 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	480	78.2	478	4	Q7Z379	Q7z379 homo sapien
2	470.5	76.6	119	4	Q9UL73	Q9ul73 homo sapien
3	469.5	76.5	492	4	Q7Z374	Q7z374 homo sapien
4	468	76.2	150	4	O95973	O95973 homo sapien
5	460	74.9	496	4	Q96KX8	Q96kx8 homo sapien
6	460	74.9	613	4	Q96EY0	Q96ey0 homo sapien
7	441	71.8	139	4	Q86SX2	Q86sx2 homo sapien
8	431	70.2	130	4	Q8IZD7	Q8izd7 homo sapien
9	429.5	70.0	588	4	Q8WUX4	Q8wux4 homo sapien
10	429.5	70.0	597	4	Q9BU10	Q9bu10 homo sapien
11	429.5	70.0	618	4	Q96AA6	Q96aa6 homo sapien
12	425.5	69.3	597	4	Q9BQB8	Q9bqb8 homo sapien
13	412	67.1	473	4	Q8TC63	Q8tc63 homo sapien
14	392.5	63.9	479	11	Q99M22	Q99m22 mus musculu
15	389	63.4	116	4	Q7Z3Y6	Q7z3y6 homo sapien
16	364	59.3	122	4	Q9UL75	Q9ul75 homo sapien
17	344.5	56.1	121	4	Q9UL96	Q9ul96 homo sapien
18	343	55.9	118	11	Q811U5	Q811u5 mus musculu
19	340	55.4	121	11	Q99NG4	Q99ng4 mus musculu
20	336	54.7	482	11	Q91X92	Q91x92 mus musculu
21	314.5	51.2	118	4	Q9UL74	Q9ul74 homo sapien
22	298.5	48.6	493	4	Q8NCL6	Q8ncl6 homo sapien
23	295	48.0	484	11	Q8VEA0	Q8vea0 mus musculu
24	295	48.0	613	4	Q8WUK1	Q8wuk1 homo sapien
25	294.5	48.0	116	4	Q9UL93	Q9ul93 homo sapien
26	291.5	47.5	113	4	Q9UL90	Q9ul90 homo sapien
27	291.5	47.5	597	4	Q96BB9	Q96bb9 homo sapien
28	290	47.2	118	4	Q9UL72	Q9ul72 homo sapien
29	288.5	47.0	481	11	Q91WT1	Q91wt1 mus musculu
30	287	46.7	147	4	Q9Y509	Q9y509 homo sapien
31	285	46.4	118	4	Q9UL91	Q9ul91 homo sapien
32	284.5	46.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
33	283	46.1	145	11	Q924P7	Q924p7 mus musculu
34	283	46.1	145	11	Q924R1	Q924r1 mus musculu
35	282	45.9	145	11	Q924R4	Q924r4 mus musculu
36	280.5	45.7	121	4	Q9UL71	Q9ul71 homo sapien
37	280.5	45.7	486	11	Q91Z07	Q91z07 mus musculu
38	280	45.6	469	11	Q8R3V9	Q8r3v9 mus musculu
39	277	45.1	124	6	Q9N0W6	Q9n0w6 oryctolagus
40	277	45.1	298	11	Q9QYF0	Q9qyf0 mus musculu
41	276.5	45.0	117	11	Q9QXE9	Q9qxe9 mus musculu
42	276	45.0	124	6	Q9N0W4	Q9n0w4 oryctolagus
43	276	45.0	143	11	Q924R0	Q924r0 mus musculu
44	275.5	44.9	499	4	Q8N5K4	Q8n5k4 homo sapien
45	275	44.8	494	4	Q96K68	Q96k68 homo sapien

ALIGNMENTS

RESULT 1
Q7Z379
ID Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN DKFZP686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 78.2%; Score 480; DB 4; Length 478;
Best Local Similarity 77.4%; Pred. No. 1.5e-41;
Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

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Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| || |:|||||| ||:||||:||||:||:|||||||
Db         24 ESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTYYNPSL 83

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGY--TLDNWGQGTLVTVSS 114
              :||:::|:|||||  |||||:|:|||||||:|||  |     | |||||:|||||
Db         84 ESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVGLGTAFDIWGQGTVVTVSS 138
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RESULT 2
Q9UL73

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ID   Q9UL73      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13219 MW;  1BDB86B6420EA0BE CRC64;

  Query Match             76.6%;  Score 470.5;  DB 4;  Length 119;
  Best Local Similarity   79.3%;  Pred. No. 2.6e-41;
  Matches   92;  Conservative    8;  Mismatches   11;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||||||||||||||||:||:| | |||
Db          6 ESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYTPSL 63

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG---YTLDNWGQGTLVTVSS 114
              |||||:||| ||| |||:|:|:|||||||:|||      |  | ||||||||||
Db         64 KSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNWGPYYFDYWGQGTLVTVSS 119


RESULT 3
Q7Z374
ID   Q7Z374      PRELIMINARY;      PRT;   492 AA.
AC   Q7Z374;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686C02218 (Fragment).
GN   DKFZP686C02218.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538077; CAD98001.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   492 AA;  53776 MW;  1E7A15760F0CA74B CRC64;

  Query Match             76.5%;  Score 469.5;  DB 4;  Length 492;
  Best Local Similarity   76.9%;  Pred. No. 2e-40;
  Matches   90;  Conservative   10;  Mismatches   12;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||: :  ||| |||||||||||||| ||:: ||||:|||

Db         37 ESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTYYSPSL 96

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR----SDGYTLDNWGQGTLVTVSS 114
              |||:|: ||||||||||||:|||||||||||| |      |:  | ||||||||||
Db         97 KSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYGW-FDPWGQGTLVTVSS 152


RESULT 4
O95973
ID   O95973      PRELIMINARY;      PRT;   150 AA.
AC   O95973;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH4 heavy chain variable region precursor (Fragment).
GN   IGM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT   "Clonal proliferation of IgM secreting B cell in the synovium of
RT   Behcet's patient with arthritis.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF103795; AAC79084.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   >150       VH4 HEAVY CHAIN VARIABLE REGION.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16315 MW;  85664E04938AA7C9 CRC64;

  Query Match             76.2%;  Score 468;  DB 4;  Length 150;
  Best Local Similarity   78.8%;  Pred. No. 6.4e-41;
  Matches   89;  Conservative    8;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:||||:||||||| |  ||| |||||| ||||||| :::||: ||||||
Db         25 ESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDYYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||||:||||||| ||||||||||||||||||      | || ||:|||||
Db         85 KSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTMVTVSS 137


RESULT 5
Q96KX8
ID   Q96KX8      PRELIMINARY;      PRT;   496 AA.
AC   Q96KX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016369; AAH16369.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
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DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53391 MW;  D346929849040D69 CRC64;

  Query Match             74.9%;  Score 460;  DB 4;  Length 496;
  Best Local Similarity   75.0%;  Pred. No. 1.9e-39;
  Matches   90;  Conservative    8;  Mismatches   14;  Indels    8;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||| |:|||||||||||||| |  ||| ||||||||||||    |:|| |||||||
Db         25 ESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITYYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-------LDNWGQGTLVTVSS 114
              |||||:|||||||  ||:: |||||||||||:|||  ||:       :| ||||||||||
Db         85 KSRVTISVDTSKNQLSLKVRSVTAADTAVYFCAR-HGYSRSGRTGAIDYWGQGTLVTVSS 143


RESULT 6
Q96EY0
ID   Q96EY0      PRELIMINARY;      PRT;   613 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67273 MW;  31214203FB8421E7 CRC64;

  Query Match             74.9%;  Score 460;  DB 4;  Length 613;
  Best Local Similarity   80.5%;  Pred. No. 2.5e-39;
  Matches   95;  Conservative    4;  Mismatches   11;  Indels    8;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  ||||||||| |||||||| || ||:| |||||
Db         25 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDN-----WGQGTLVTVSS 114
              |||||||||||| |||:|||||||||||||| |  : |        ||||||||||
Db         83 KSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCA-SQPWELPTVGLFYWGQGTLVTVSS 139


RESULT 7
Q86SX2
ID   Q86SX2      PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)
DE   of Homo sapiens (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Plasmid.
FT   NON_TER       1       1
SQ   SEQUENCE   139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;

  Query Match             71.8%;  Score 441;  DB 4;  Length 139;
  Best Local Similarity   89.4%;  Pred. No. 3.8e-38;
  Matches   84;  Conservative    5;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||||||||||| |  |||||||||||||||||||:||:| |||||
Db         38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 95

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR 95
              |||||:||||||| |||:||||||||||||||||
Db         96 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129


RESULT 8
Q8IZD7
ID   Q8IZD7      PRELIMINARY;      PRT;   130 AA.
AC   Q8IZD7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-thyroglobulin heavy chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jang Y.-J., Chung J., Park J.-Y.;
RT   "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT   Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145445; AAN64329.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     130     130
SQ   SEQUENCE   130 AA;  13901 MW;  036131FC6EC1551E CRC64;

  Query Match             70.2%;  Score 431;  DB 4;  Length 130;
  Best Local Similarity   71.2%;  Pred. No. 3.8e-37;
  Matches   89;  Conservative    8;  Mismatches   16;  Indels   12;  Gaps    4;
```

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNT-----Y 56
              :|||||||||:|||||||||||||| |  ||| |||| |||||||| :|:||:|     |
Db          6 QSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTYSGSPY 65

Qy         57 YNPSLKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR----SDG--YT-LDNWGQGTL 109
              | |||:||| :|||||||  |||||||||||||||||     | |  |    :|||| |
Db         66 YAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFQHWGQGFL 125

Qy        110 VTVSS 114
              |||||
Db        126 VTVSS 130
```

RESULT 9
Q8WUX4
ID Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 70.0%; Score 429.5; DB 4; Length 588;
Best Local Similarity 72.5%; Pred. No. 3.6e-36;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

```
Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||||||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |||:||||||   ||:|||| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144
```

RESULT 10
Q9BU10
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 70.0%; Score 429.5; DB 4; Length 597;
Best Local Similarity 72.5%; Pred. No. 3.7e-36;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

```
Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||||||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |||:||||||   ||:|||| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144
```

RESULT 11
Q96AA6
ID Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC017356; AAH17356.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 70.0%; Score 429.5; DB 4; Length 618;
Best Local Similarity 72.5%; Pred. No. 3.8e-36;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

```
Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||||||||||||||| | |||:| |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 84

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |||:||||||   ||:|||| ||||||||||        :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144
```

RESULT 12
Q9BQB8
ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle, and Lymph;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;

  Query Match             69.3%;  Score 425.5;  DB 4;  Length 597;
  Best Local Similarity   72.5%;  Pred. No. 9.6e-36;
  Matches   87;  Conservative    6;  Mismatches   16;  Indels   11;  Gaps    3;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:|||:|||||| | |||    ||||||||||||||||||| | ||| | |||||||
Db         27 GAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGITNYNPSLKS 84

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--------SDG-YTLDNWGQGTLVTVSS 114
              |||:||||||    ||:|||| ||||||||||         :|| | :| ||||| |||||
Db         85 RVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQGTTVTVSS 144


RESULT 13
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   GO; GO:0005507; F:copper ion binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match             67.1%;  Score 412;  DB 4;  Length 473;
  Best Local Similarity   69.0%;  Pred. No. 1.8e-34;
  Matches   80;  Conservative   11;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||:||| |||||||||| |: |  ||| |:|||||||||||| |  ||| ||:|||
Db         32 ESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQPPGKGLEWIGTINFSGNMYYSPSL 91

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTL----DNWGQGTLVTVS 113
              :|||||| | |:| | |:| ||||||||||||||    |: :     :|||| ||:||
Db         92 RSRVTMSADMSENSFYLKLDSVTAADTAVYYCAA--GHLVMGFGAHWGQGKLVSVS 145


RESULT 14
Q99M22
ID   Q99M22      PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768E39A138918892 CRC64;

  Query Match             63.9%;  Score 392.5;  DB 11;  Length 479;
  Best Local Similarity   67.5%;  Pred. No. 2e-32;
  Matches   77;  Conservative   16;  Mismatches   18;  Indels    3;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||:|:| || | ||||:|||| ||  |||:||| : |:  |||||
Db         24 ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWMGYINYDGSNNYNPSL 82

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGTLVTVSS 114
              |:|:::: ||||| | |:|:|||  ||| |||| | ||:   ||||||||||:
Db         83 KNRISITRDTSKNQFFLKLNSVTTEDTATYYCA-SRGYSWFPNWGQGTLVTVSA 135


RESULT 15
Q7Z3Y6
ID   Q7Z3Y6      PRELIMINARY;      PRT;   116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   VH4-34.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RT   "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT   indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT   cell precursor in a germinal center.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
FT   NON_TER       1       1
```

```
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A846616C908 CRC64;

  Query Match             63.4%;  Score 389;  DB 4;  Length 116;
  Best Local Similarity   68.5%;  Pred. No. 7.9e-33;
  Matches   76;  Conservative    9;  Mismatches   14;  Indels   12;  Gaps    2;

Qy          4 GPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLKS 63
              | ||:|||:||||:| | |||    ||||:||||||||||||| | |||:| ||||||
Db          8 GAGLLKPSETLSLSCAVYGGSF--SGYYWNWIRQPPGKGLEWIGEINHSGSTNYNPSLKS 65

Qy         64 RVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD----------GYTLDNW 104
              |||:|||||||  ||:|||||||||||||||| :          | :| |
Db         66 RVTISVDTSKNQLSLKLSSVTAADTAVYYCARGEIVVVPAASYYYYYMDVW 116


Search completed: August  8, 2004, 12:17:45
Job time : 32.2636 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605	98.5	114	5	ABG30447	Abg30447 Human IgE
2	600	97.7	114	5	ABG30446	Abg30446 Human IgE
3	556	90.6	114	5	ABG30445	Abg30445 Human IgE
4	521	84.9	473	4	AAB36206	Aab36206 Human imm
5	516.5	84.1	123	2	AAW78433	Aaw78433 Antibody
6	516.5	84.1	123	5	ABB97976	Abb97976 Heavy cha
7	515.5	84.0	117	7	ADC99784	Adc99784 Anti-huma
8	515.5	84.0	117	7	ADD05388	Add05388 Anti-MUC1
9	513.5	83.6	120	4	AAB62775	Aab62775 Human HIV
10	512	83.4	123	4	AAB62745	Aab62745 Human HIV
11	510.5	83.1	122	4	AAB62765	Aab62765 Human HIV
12	510	83.1	246	3	AAY15126	Aay15126 Anti-muri
13	508	82.7	172	3	AAY93713	Aay93713 The heavy
14	508	82.7	172	6	AAE35892	Aae35892 Human 2.1
15	507.5	82.7	117	7	ADC99776	Adc99776 Anti-huma
16	507.5	82.7	117	7	ADD05380	Add05380 Anti-MUC1
17	507	82.6	126	3	AAB30584	Aab30584 A human v
18	507	82.6	126	5	ABP54970	Abp54970 Anti-idio
19	507	82.6	251	5	ABG80712	Abg80712 Amyloid p
20	507	82.6	252	5	ABP45983	Abp45983 Human BLy
21	507	82.6	254	5	ABG80713	Abg80713 Amyloid p
22	507	82.6	263	5	ABG80714	Abg80714 Human IgG
23	506.5	82.5	251	6	ABJ19829	Abj19829 Human VEG
24	506.5	82.5	253	5	ABP45608	Abp45608 Human BLy
25	503	81.9	252	5	ABP45318	Abp45318 Human BLy
26	502.5	81.8	119	2	AAW27554	Aaw27554 Human Ab
27	502.5	81.8	119	6	ABJ18676	Abj18676 Antibody
28	502.5	81.8	127	4	AAG80217	Aag80217 Human aut
29	502	81.8	118	2	AAY06385	Aay06385 Humanised
30	502	81.8	139	3	AAY56713	Aay56713 Amino aci
31	501	81.6	130	5	AAU81273	Aau81273 Human trk
32	501	81.6	256	5	ABP45596	Abp45596 Human BLy
33	497.5	81.0	119	7	ADC99796	Adc99796 Anti-huma
34	497.5	81.0	119	7	ADD05400	Add05400 Anti-MUC1
35	496	80.8	121	5	ABB07171	Abb07171 ebvHigM M
36	495.5	80.7	121	7	ADE28455	Ade28455 Human ant
37	495.5	80.7	123	6	ADA89258	Ada89258 Human ant
38	495.5	80.7	129	5	AAU81275	Aau81275 Human trk
39	495.5	80.7	466	7	ADE28479	Ade28479 Human ant
40	495	80.6	118	2	AAY06383	Aay06383 Humanised
41	494.5	80.5	121	7	ADC99808	Adc99808 Anti-huma
42	494.5	80.5	121	7	ADD05412	Add05412 Anti-MUC1
43	494.5	80.5	251	5	ABP44979	Abp44979 Human BLy
44	493.5	80.4	121	7	ADE28491	Ade28491 Human ant
45	493.5	80.4	466	7	ADE28471	Ade28471 Human ant

ALIGNMENTS

RESULT 1
ABG30447
ID ABG30447 standard; protein; 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89639.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 38; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 100 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 98.5%; Score 605; DB 5; Length 114;
Best Local Similarity 99.1%; Pred. No. 2.6e-44;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 2
ABG30446
ID ABG30446 standard; protein; 114 AA.
XX
AC ABG30446;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .26
FT		/note= "FR1 region"
FT	Region	27. .33
FT		/note= "CDR1 region"
FT	Region	34. .47
FT		/note= "FR2 region"
FT	Region	48. .63
FT		/note= "CDR2 protein"
FT	Region	64. .95
FT		/note= "FR3 region"
FT	Region	96. .103
FT		/note= "CDR2 region"
FT	Region	104. .114
FT		/note= "FR4 region"

XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89638.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 37; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 97.7%; Score 600; DB 5; Length 114;
Best Local Similarity 96.5%; Pred. No. 6.9e-44;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||||||||||||||||||||||||:|||||||||||| ||||||||||||
Db          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWVRQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||:||||||||||||||:||||||||||||||||||||||||||||||||||||
Db         61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
```

RESULT 3
ABG30445
ID ABG30445 standard; protein; 114 AA.
XX
AC ABG30445;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 94 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .26
FT		/note= "FR1 region"
FT	Region	27. .33
FT		/note= "CDR1 region"
FT	Region	34. .47
FT		/note= "FR2 region"
FT	Region	48. .63
FT		/note= "CDR2 protein"
FT	Region	64. .95
FT		/note= "FR3 region"

FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"
XX
PN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89637.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 36; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to PhI p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to PhI p 2. The present sequence represents the human IgG
CC fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 114 AA;

Query Match 90.6%; Score 556; DB 5; Length 114;
Best Local Similarity 90.4%; Pred. No. 4e-40;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
              ||||||||||:|||||:| |||||||||||||||||| ||||||||||||||||||||||
Db          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||: ||||||:| |||||:|||||||||||||| |||||| ||||||||||
Db         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114
```

RESULT 4
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-4.
XX
KW Human; immune system associated protein; HISAP-4; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR N-PSDB; AAC66522.
XX
PT New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
PS Claim 1; Col 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 473 AA;

Query Match 84.9%; Score 521; DB 4; Length 473;
Best Local Similarity 83.2%; Pred. No. 1.7e-36;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

```
Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||| |||||| ||||||||||||||||||||||:||:| |||||
Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD------GYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||| |       | :| ||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143
```

RESULT 5
AAW78433
ID AAW78433 standard; protein; 123 AA.
XX
AC AAW78433;
XX
DT 11-MAY-1999 (first entry)
XX
DE Antibody heavy chain targeted to obr clone 26.
XX
KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
XX
OS Synthetic.
XX
PN WO9850431-A2.
XX
PD 12-NOV-1998.
XX
PF 30-APR-1998; 98WO-US008762.
XX
PR 02-MAY-1997; 97US-00850058.
PR 24-JUN-1997; 97US-0050661P.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon R, Carter PJ, Merchant AM, Presta LG;

XX
DR WPI; 1999-070091/06.
XX
PT Selective preparation of multispecific antibodies - with heteromultimeric
PT heavy chain and common light chain components, useful for, e.g. in vivo
PT diagnosis of cancer.
XX
PS Example 4; Fig 5; 69pp; English.
XX
CC This sequence represents the heavy chain variable region for an antibody
CC that binds to the obr clone 26 protein. The sequence encoding the chain
CC is generated by a new method for preparing a multispecific Ab comprising
CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP
CC comprises a multimerisation domain (MD) forming an interface positioned
CC to interact with an interface of a MD of the extra PP; and (ii) the first
CC and extra PPs each have a binding domain, which comprises a heavy chain
CC and a light chain, where the variable light chains of the first and extra
CC PPs comprise a common sequence. The method comprises: (a) culturing a
CC host cell comprising nucleic acid encoding the first PP and extra PP, and
CC the variable light chain, such that the nucleic acid is expressed; and
CC (b) recovering the multispecific Ab from the culture. The method prepares
CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins
CC and Ab-immunoadhesin chimeras. The method allows for the enhanced
CC formation of the desired heteromultimer relative to the undesired
CC heteromultimers and homomultimers. The Abs can be used in immunoassays
CC and for the in vitro or in vivo diagnosis of various diseases, such as
CC cancer
XX
SQ Sequence 123 AA;

Query Match 84.1%; Score 516.5; DB 2; Length 123;
Best Local Similarity 84.0%; Pred. No. 1e-36;
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
              :|||||||||||||||||||||| |||||||||| ||||||||||||:||:||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              ||||||:||||||| |||:|||||||||||||||| |         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 6
ABB97976
ID ABB97976 standard; protein; 123 AA.
XX
AC ABB97976;
XX
DT 06-SEP-2002 (first entry)
XX
DE Heavy chain variable region from antibody obr.26.
XX
KW Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
KW antiviral; vaccine; tumour.
XX
OS Synthetic.
XX
PN US2002062010-A1.
XX
PD 23-MAY-2002.
XX
PF 23-MAY-2001; 2001US-00863693.
XX
PR 02-MAY-1997; 97US-0046816P.
PR 30-APR-1998; 98US-00070166.
XX
PA (GETH) GENENTECH INC.
XX
PI Arathoon WR, Carter PJ, Merchant AM, Presta LG;
XX
DR WPI; 2002-499676/53.
XX
PT New multispecific antibodies having heteromultimeric and common
PT components are useful to direct treatment to a target site such as a
PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
PT treat infectious disease.
XX
PS Example 4; Fig 5; 36pp; English.
XX
CC The invention relates to a new multispecific antibody, comprising at
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1
CC has a multimerisation domain forming an interface positioned to interact
CC with an interface of a multimerisation domain of PP2, and both
CC polypeptides each comprise a binding domain consisting a heavy chain and
CC a variable light chain, where the light chain has a sequence common to
CC both polypeptides. Hetromultimers of the inventions include bispecific
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin
CC chimeras. The activity of antibodies of the invention may be described
CC as, cytostatic, antibacterial and antiviral. The heteromultimer can be
CC used for redirected cytotoxicity, for example to kill tumour cells, as a
CC vaccine adjuvant, for delivering thrombolytic agents to clots, for
CC converting enzyme activated prodrugs at a target site such as a tumour,
CC for treating infectious diseases, for targeting immune complexes to cell
CC surface receptors or for delivering immunotoxins to tumour cells. The
CC current sequence represents the heavy chain variable region from antibody
CC obr.26 used in the construction of bispecific antibodies
XX
SQ Sequence 123 AA;

Query Match 84.1%; Score 516.5; DB 5; Length 123;
Best Local Similarity 84.0%; Pred. No. 1e-36;
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

```
Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
              :|||||||||||||||||||||| |||||||||| ||||||||||||:||:||||||
Db          5 VESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS 64

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYTLDNWGQGTLVTVSS 114
              ||||||:||||||| |||:|||||||||||||||| |         | ||||||||||
Db         65 LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVDLEDYGSGASDYWGQGTLVTVSS 123
```

RESULT 7
ADC99784
ID ADC99784 standard; protein; 117 AA.
XX
AC ADC99784;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99786.
XX
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 1; SEQ ID NO 13; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 84.0%; Score 515.5; DB 7; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.2e-36;
Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117

RESULT 8
ADD05388
ID ADD05388 standard; protein; 117 AA.
XX
AC ADD05388;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR N-PSDB; ADD05390.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 1; SEQ ID NO 13; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
CC protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 84.0%; Score 515.5; DB 7; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.2e-36;
Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF--DYWGQGTLVTVSS 117

RESULT 9
AAB62775
ID AAB62775 standard; protein; 120 AA.
XX
AC AAB62775;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR N-PSDB; AAF29076.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
PS Claim 1; Page 69; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ Sequence 120 AA;

Query Match 83.6%; Score 513.5; DB 4; Length 120;
Best Local Similarity 86.2%; Pred. No. 1.8e-36;

```
  Matches  100;  Conservative    5;  Mismatches    6;  Indels    5;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| ||||||||||||:||:|||||||
Db          7 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 66

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:||||||||||||||||     | :  | ||||||||||
Db         67 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVVVDWF--DPWGQGTLVTVSS 120


RESULT 10
AAB62745
ID   AAB62745 standard; protein; 123 AA.
XX
AC   AAB62745;
XX
DT   03-APR-2001  (first entry)
XX
DE   Human HIV-1 monoclonal antibody SEQ ID NO: 44.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200100678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US017327.
XX
PR   30-JUN-1999;   99US-0141701P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   N-PSDB; AAF29046.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal.
XX
PS   Claim 1; Page 50; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ   Sequence 123 AA;

  Query Match             83.4%;  Score 512;  DB 4;  Length 123;
  Best Local Similarity   83.8%;  Pred. No. 2.5e-36;
  Matches   98;  Conservative    7;  Mismatches    8;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| ||||||||||||:||:|||||||
Db          7 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYNSGSTYYNPSL 66

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS----DGYTLDNWGQGTLVTVSS 114
              |||||:|:||||| |||:||||||||||||||:       : | ||||||||||
Db         67 KSRVTISIDTSKNKFSLKLSSVTAADTAVYYCARAAYCGGDCSFDYWGQGTLVTVSS 123


RESULT 11
AAB62765
ID   AAB62765 standard; protein; 122 AA.
XX
AC   AAB62765;
XX
DT   03-APR-2001  (first entry)
XX
DE   Human HIV-1 monoclonal antibody SEQ ID NO: 64.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200100678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US017327.
XX
PR   30-JUN-1999;   99US-0141701P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   N-PSDB; AAF29066.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal.
XX
PS   Claim 1; Page 63; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ   Sequence 122 AA;

  Query Match             83.1%;  Score 510.5;  DB 4;  Length 122;
  Best Local Similarity   85.3%;  Pred. No. 3.3e-36;
  Matches   99;  Conservative    5;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| ||||||||||||:||:|||||||
Db          7 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 66

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:||||||||||||||:     |    |  ||:||||||||
Db         67 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDMLRDSTGLCYWGRGTLVTVSS 122


RESULT 12
AAY15126
ID   AAY15126 standard; protein; 246 AA.
XX
AC   AAY15126;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Anti-murine CTLA-4 M3 sFv.
XX
KW   Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;
KW   membrane-associated protein; chimeric construct; extracellular domain;
KW   human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
KW   recipient CD28; T-cell proliferation;
KW   xenograft-specific immunosuppression.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9957266-A2.
XX
```

PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-GB001350.
XX
PR 30-APR-1998; 98GB-00009280.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Lechler IR, Dorling A;
XX
DR WPI; 2000-038815/03.
DR N-PSDB; AAZ28998.
XX
PT Inhibiting T-cell mediated rejection of xenotransplanted organs.
XX
PS Claim 9; Fig 11; 43pp; English.
XX
CC The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC comprising DNA sequences encoding the extracellular domain of murine
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated
CC T-cells and antagonises the co-stimulatory signal provided by the
CC interaction between donor B7 and recipient CD28. Cells expressing the
CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
CC xenograft-specific immunosuppression
XX
SQ Sequence 246 AA;

Query Match 83.1%; Score 510; DB 3; Length 246;
Best Local Similarity 85.0%; Pred. No. 7.6e-36;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
Db 8 ESGPGLVKPSETLSLTCTVSGGSVSSGSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSL 67

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
Db 68 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMRKDKFDYWGQGTLVTVSS 120

RESULT 13
AAY93713
ID AAY93713 standard; protein; 172 AA.
XX
AC AAY93713;
XX
DT 03-OCT-2000 (first entry)
XX
DE The heavy chain of immunoglobulin clone 2.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.
XX
OS Homo sapiens.
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR WPI; 2000-442647/38.
DR N-PSDB; AAA46876.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
PS Claim 2; Fig 1G; 157pp; English.
XX
CC The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 172 AA;

Query Match 82.7%; Score 508; DB 3; Length 172;
Best Local Similarity 85.1%; Pred. No. 7.8e-36;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLK 62
Db 1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy 63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114

RESULT 14
AAE35892
ID AAE35892 standard; protein; 172 AA.
XX
AC AAE35892;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human 2.1.3 anti-CTLA-4 antibody heavy chain.
XX
KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24. .31
FT /note= "Complementarity determining region (CDR) 1"
FT Region 45. .61
FT /note= "Complementarity determining region (CDR) 2"
FT Region 94. .103
FT /note= "Complementarity determining region (CDR) 3"
XX
PN EP1262193-A1.
XX
PD 04-DEC-2002.
XX
PF 23-MAY-2002; 2002EP-00253652.
XX
PR 23-MAY-2001; 2001US-0293042P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Hanson DC, Mueller EE;
XX
DR WPI; 2003-131215/13.
XX
PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the

```
PT   preparation of medicament for the treatment of cancer.
XX
PS   Disclosure; Fig 3; 76pp; English.
XX
CC   The invention relates to the use of human anti-cytotoxic T lymphocyte
CC   antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC   the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC   cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC   cancer, cancer of the anal region, stomach cancer, breast cancer,
CC   testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC   The present sequence is human anti-CTLA-4 antibody heavy chain
XX
SQ   Sequence 172 AA;

  Query Match             82.7%;  Score 508;  DB 6;  Length 172;
  Best Local Similarity   85.1%;  Pred. No. 7.8e-36;
  Matches   97;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLK 62
              |||||||||| |||||||||||| |||:||||||| |||||||||||: ||||||||||
Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              ||||:||||||| |||:|||||||||||||||  |  | :| ||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 15
ADC99776
ID   ADC99776 standard; protein; 117 AA.
XX
AC   ADC99776;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.
XX
KW   anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW   cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW   cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW   lung cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO2003057838-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041581.
XX
PR   28-DEC-2001; 2001US-0346299P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Gudas J;
XX
DR   WPI; 2003-587113/55.
DR   N-PSDB; ADC99778.
XX
PT   New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT   or condition associated with expression of MUC18 in a patient, e.g.
PT   tumors, cancers, and other malignancies.
XX
PS   Claim 1; SEQ ID NO 5; 78pp; English.
XX
CC   The invention relates to a novel isolated monoclonal antibody comprising
CC   a heavy or light chain amino acid or a heavy or light chain variable
CC   domain where the antibody binds to MUC18. The monoclonal antibody of the
CC   invention demonstrates cytostatic activity and may be useful for treating
CC   a disease or condition associated with the expression of MUC18 on the
CC   cell surface such as tumours, specifically melanoma, oesophageal,
CC   pancreatic or colorectal tumours, carcinomas, particularly cervical
CC   carcinomas and cervical intraepithelial neoplasia and cancers including
CC   colorectal, breast or lung cancer, as well as other malignancies. The
CC   current sequence is that of the anti-human MUC18 monoclonal antibody
CC   heavy chain protein of the invention.
XX
SQ   Sequence 117 AA;

  Query Match             82.7%;  Score 507.5;  DB 7;  Length 117;
  Best Local Similarity   86.8%;  Pred. No. 5.8e-36;
  Matches   99;  Conservative    5;  Mismatches    7;  Indels    3;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| || |:|||||| |||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-SDGYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||  |||    ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKY--WGQGTLVTVSS 117


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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
928.389 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	614	100.0	114	14	US-10-027-725A-9	Sequence 9, Appli
2	600	97.7	114	14	US-10-027-725A-8	Sequence 8, Appli
3	556	90.6	114	14	US-10-027-725A-7	Sequence 7, Appli
4	524.5	85.4	121	15	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	15	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	15	US-10-309-762-10	Sequence 10, Appl
7	521	84.9	120	15	US-10-309-762-13	Sequence 13, Appl
8	521	84.9	120	15	US-10-309-762-144	Sequence 144, App
9	521	84.9	122	15	US-10-309-762-147	Sequence 147, App
10	520	84.7	221	10	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	15	US-10-309-762-151	Sequence 151, App
12	519.5	84.6	125	15	US-10-309-762-11	Sequence 11, Appl
13	517.5	84.3	119	15	US-10-309-762-140	Sequence 140, App
14	516.5	84.1	123	15	US-10-309-762-12	Sequence 12, Appl
15	516	84.0	124	15	US-10-309-762-75	Sequence 75, Appl
16	516	84.0	143	15	US-10-309-762-96	Sequence 96, Appl
17	515.5	84.0	117	14	US-10-330-613-13	Sequence 13, Appl
18	515.5	84.0	117	14	US-10-330-530-13	Sequence 13, Appl
19	515.5	84.0	117	16	US-10-660-357-13	Sequence 13, Appl
20	514	83.7	120	15	US-10-309-762-128	Sequence 128, App
21	514	83.7	120	15	US-10-309-762-139	Sequence 139, App
22	514	83.7	121	12	US-10-453-698-137	Sequence 137, App
23	514	83.7	121	15	US-10-308-817-137	Sequence 137, App
24	513	83.6	116	15	US-10-309-762-127	Sequence 127, App
25	512.5	83.5	125	15	US-10-309-762-8	Sequence 8, Appli
26	512.5	83.5	125	15	US-10-309-762-16	Sequence 16, Appl
27	511.5	83.3	119	15	US-10-309-762-131	Sequence 131, App
28	511	83.2	110	15	US-10-309-762-74	Sequence 74, Appl
29	510.5	83.1	123	15	US-10-309-762-9	Sequence 9, Appli
30	510.5	83.1	127	15	US-10-309-762-14	Sequence 14, Appl
31	508.5	82.8	125	15	US-10-309-762-153	Sequence 153, App
32	508	82.7	172	14	US-10-153-382-21	Sequence 21, Appl
33	507.5	82.7	117	14	US-10-330-613-5	Sequence 5, Appli
34	507.5	82.7	117	14	US-10-330-530-5	Sequence 5, Appli
35	507.5	82.7	117	16	US-10-660-357-5	Sequence 5, Appli
36	507.5	82.7	123	15	US-10-309-762-17	Sequence 17, Appl
37	507	82.6	126	9	US-09-974-449-6	Sequence 6, Appli
38	507	82.6	252	10	US-09-880-748-1994	Sequence 1994, Ap
39	507	82.6	252	12	US-10-293-418-1994	Sequence 1994, Ap
40	506.5	82.5	119	15	US-10-309-762-143	Sequence 143, App
41	506.5	82.5	251	14	US-10-120-414-75	Sequence 75, Appl
42	506.5	82.5	253	10	US-09-880-748-1619	Sequence 1619, Ap
43	506.5	82.5	253	12	US-10-293-418-1619	Sequence 1619, Ap
44	505.5	82.3	123	15	US-10-309-762-18	Sequence 18, Appl
45	505.5	82.3	123	15	US-10-309-762-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match 100.0%; Score 614; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPS 60
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Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
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RESULT 2
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:

```
;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-8

  Query Match             97.7%;  Score 600;  DB 14;  Length 114;
  Best Local Similarity   96.5%;  Pred. No. 3e-47;
  Matches  110;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||:|||||||||||| ||||||||||||
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Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||:|||||||||||||||:||||||||||||||||||||||||||||||||
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RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
;  APPLICANT: Flicker, Sabine
;  TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
;  FILE REFERENCE: 25401-4
;  CURRENT APPLICATION NUMBER: US/10/027,725A
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/259,436
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-027-725A-7

  Query Match             90.6%;  Score 556;  DB 14;  Length 114;
  Best Local Similarity   90.4%;  Pred. No. 3.1e-43;
  Matches  103;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

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              ||||||||||:|||||:| ||||||||||||||||| ||||||||||||||||||||
Db          1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYYWSWIRQHPGKGLEWIGYIYHSGNTYYNPS 60

Qy         61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              ||||: |||||||:| |||||:|||||||||||||| |||||| ||||||||||
Db         61 LKSRIAMSVDTSENKFSLRLNSVTAADTAVYYCARLDGYTLDIWGQGTLVTVSS 114


RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-152

  Query Match             85.4%;  Score 524.5;  DB 15;  Length 121;
  Best Local Similarity   86.2%;  Pred. No. 2.5e-40;
  Matches  100;  Conservative    5;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD---GYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||  |   ||  | |||||:|||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAYYDILTGYAFDIWGQGTMVTVSS 121


RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-138

  Query Match             85.3%;  Score 524;  DB 15;  Length 118;
  Best Local Similarity   88.5%;  Pred. No. 2.7e-40;
  Matches  100;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||| |   | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYGSGSDYWGQGTLVTVSS 118


RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
```

```
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-10

  Query Match             85.3%;  Score 523.5;  DB 15;  Length 123;
  Best Local Similarity   85.6%;  Pred. No. 3.1e-40;
  Matches  101;  Conservative    5;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS-----DGYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||:      |   || ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARAGKYYGSGSYLDYWGQGTLVTVSS 123


RESULT 7
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-13

  Query Match             84.9%;  Score 521;  DB 15;  Length 120;
  Best Local Similarity   87.1%;  Pred. No. 5.1e-40;
  Matches  101;  Conservative    5;  Mismatches    6;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT---LDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||| |||     | ||:||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 8
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-144

  Query Match             84.9%;  Score 521;  DB 15;  Length 120;
  Best Local Similarity   87.1%;  Pred. No. 5.1e-40;
  Matches  101;  Conservative    5;  Mismatches    6;  Indels    4;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT---LDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||| |||     | ||:||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-DGYNYWYFDLWGRGTLVTVSS 120


RESULT 9
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-147

  Query Match             84.9%;  Score 521;  DB 15;  Length 122;
  Best Local Similarity   85.5%;  Pred. No. 5.2e-40;
  Matches  100;  Conservative    5;  Mismatches    8;  Indels    4;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||||| |||||||||| ||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR----SDGYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||||||      || :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYDILTGYGMDVWGQGTTVTVSS 122


RESULT 10
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
;  APPLICANT: Deshpande, Rajendra
;  APPLICANT:  Tsai, Mei-Mei
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
```

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;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: US/09/972,656
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-972-656-80

  Query Match             84.7%;  Score 520;  DB 10;  Length 221;
  Best Local Similarity   86.7%;  Pred. No. 1.2e-39;
  Matches   98;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||:|||||| |||||| |||| |||||||||||||||||||||:|||||||
Db          6 ESGPGLVKPSETLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIGYIYHSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGTLVTVSS 114
              |||||:||| ||| |||:||||||||||||||| |    | ||||||||||
Db         66 KSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARGDWGYFDYWGQGTLVTVSS 118


RESULT 11
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-151

  Query Match             84.6%;  Score 519.5;  DB 15;  Length 121;
  Best Local Similarity   86.2%;  Pred. No. 7.1e-40;
  Matches  100;  Conservative    5;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              ||||||||||||||||||||||| |||||||||| |||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS---DGYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||  -   || :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVLLWFGYGMDVWGQGTTVTVSS 121


RESULT 12
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-11

  Query Match             84.6%;  Score 519.5;  DB 15;  Length 125;
  Best Local Similarity   83.3%;  Pred. No. 7.3e-40;
  Matches  100;  Conservative    6;  Mismatches    7;  Indels    7;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||| |||||||||| |||||||||||:||||||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGNTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARS-----DGY--TLDNWGQGTLVTVSS 114
              |||:|:||||||| |||:|||||||||||||||:      ||    | |||||:|||||
Db         66 KSRITISVDTSKNQFSLKLSSVTAADTAVYYCARTYYDFLTGYPDAFDIWGQGTMVTVSS 125


RESULT 13
US-10-309-762-140
; Sequence 140, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 140
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-140

  Query Match             84.3%;  Score 517.5;  DB 15;  Length 119;
  Best Local Similarity   86.8%;  Pred. No. 1.1e-39;
  Matches   99;  Conservative    6;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||| |||||||||| |||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-GYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||  :  | :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGNYYYGMDVWGQGTTVTVSS 119


RESULT 14
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
```

```
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-12

  Query Match             84.1%;  Score 516.5;  DB 15;  Length 123;
  Best Local Similarity   83.9%;  Pred. No. 1.4e-39;
  Matches   99;  Conservative    5;  Mismatches    9;  Indels    5;  Gaps    1;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| |||||||||||:|| |||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGTTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDGYTLDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||      : | :| ||||| |||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVLLWFGEDYGVDVWGQGTTVTVSS 123


RESULT 15
US-10-309-762-75
; Sequence 75, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-762-75

  Query Match             84.0%;  Score 516;  DB 15;  Length 124;
  Best Local Similarity   84.0%;  Pred. No. 1.5e-39;
  Matches  100;  Conservative    6;  Mismatches    7;  Indels    6;  Gaps    2;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
              |||||||||||||||||||||||| |||||||||| |||||||||||:||:|||||||
Db          6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSL 65

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYT-LDNWGQGTLVTVSS 114
              |||||:||||||| |||:|||||||||||||||| :     |:   | ||||||||||
Db         66 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARENYDILTGFNWFDPWGQGTLVTVSS 124


Search completed: August  8, 2004, 12:43:20
Job time : 38.5182 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSLTCTV.....RSDGYTLDNWGQGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	521	84.9	473	3	US-09-049-672A-4	Sequence 4, Appli
2	508	82.7	172	4	US-09-472-087-7	Sequence 7, Appli
3	508	82.7	172	4	US-09-472-087-86	Sequence 86, Appl
4	502.5	81.8	119	4	US-09-025-769B-39	Sequence 39, Appl
5	502.5	81.8	119	4	US-09-025-769B-65	Sequence 65, Appl
6	496	80.8	122	1	US-08-360-125-11	Sequence 11, Appl
7	496	80.8	122	2	US-08-450-578-11	Sequence 11, Appl
8	496	80.8	122	2	US-09-017-628-11	Sequence 11, Appl
9	496	80.8	122	2	US-09-014-880-11	Sequence 11, Appl
10	496	80.8	122	4	US-08-450-363-11	Sequence 11, Appl
11	492	80.1	487	4	US-09-800-729-145	Sequence 145, App
12	491	80.0	118	4	US-09-025-769B-25	Sequence 25, Appl
13	487.5	79.4	119	1	US-08-360-125-5	Sequence 5, Appli
14	487.5	79.4	119	2	US-08-450-578-5	Sequence 5, Appli
15	487.5	79.4	119	2	US-09-017-628-5	Sequence 5, Appli
16	487.5	79.4	119	2	US-09-014-880-5	Sequence 5, Appli
17	487.5	79.4	119	4	US-08-450-363-5	Sequence 5, Appli
18	472	76.9	244	4	US-08-918-148-79	Sequence 79, Appl
19	467	76.1	118	3	US-08-545-809A-116	Sequence 116, App
20	466.5	76.0	142	2	US-08-480-774A-2	Sequence 2, Appli
21	463.5	75.5	250	4	US-10-039-785-50	Sequence 50, Appl
22	460.5	75.0	119	2	US-08-652-816A-10	Sequence 10, Appl
23	460	74.9	278	3	US-09-260-527-3	Sequence 3, Appli
24	457	74.4	118	3	US-08-545-809A-142	Sequence 142, App
25	457	74.4	118	4	US-09-343-698-6	Sequence 6, Appli
26	457	74.4	118	4	US-08-325-955-6	Sequence 6, Appli
27	450.5	73.4	219	4	US-09-460-384-37	Sequence 37, Appl
28	450	73.3	832	3	US-08-630-820-7	Sequence 7, Appli
29	450	73.3	832	4	US-09-273-453-7	Sequence 7, Appli
30	449	73.1	126	1	US-08-276-852-142	Sequence 142, App
31	449	73.1	126	1	US-08-899-575-142	Sequence 142, App
32	449	73.1	126	1	US-08-899-575-142	Sequence 142, App
33	449	73.1	126	5	PCT-US95-08743-142	Sequence 142, App
34	448	73.0	118	3	US-08-545-809A-123	Sequence 123, App
35	446.5	72.7	98	1	US-08-478-039-75	Sequence 75, Appl
36	446.5	72.7	98	1	US-08-476-349A-75	Sequence 75, Appl
37	446.5	72.7	123	1	US-08-137-117D-64	Sequence 64, Appl
38	446.5	72.7	123	2	US-08-436-717-64	Sequence 64, Appl
39	446.5	72.7	123	4	US-08-793-450-4	Sequence 4, Appli
40	446.5	72.7	138	1	US-08-137-117D-69	Sequence 69, Appl
41	446.5	72.7	138	2	US-08-436-717-69	Sequence 69, Appl
42	446.5	72.7	472	4	US-08-793-450-8	Sequence 8, Appli
43	444	72.3	150	4	US-09-582-337-14	Sequence 14, Appl
44	442.5	72.1	124	1	US-08-478-039-78	Sequence 78, Appl
45	442.5	72.1	124	1	US-08-476-349A-78	Sequence 78, Appl

ALIGNMENTS

```
RESULT 1
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Tang, Y. Tom
;    APPLICANT:  Yue, Henry
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Baughn, Mariah R.
;    TITLE OF INVENTION:  HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,672A
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0497 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  473 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  PANCTUT01
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;      CLONE:  1513264
US-09-049-672A-4

  Query Match             84.9%;  Score 521;  DB 3;  Length 473;
  Best Local Similarity   83.2%;  Pred. No. 1.6e-44;
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Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
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Db         25 ESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTLYNPSL 84

Qy         62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD------GYTLDNWGQGTLVTVSS 114
              |||||:|||||| |||:|||||||||||||| |       | :| ||||||||||
Db         85 KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLVTVSS 143


RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-7

  Query Match             82.7%;  Score 508;  DB 4;  Length 172;
  Best Local Similarity   85.1%;  Pred. No. 9.9e-44;
  Matches   97;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLK 62
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Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              ||||:||||||| |||:|||||||||||||||  |  | :| ||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-86

  Query Match             82.7%;  Score 508;  DB 4;  Length 172;
  Best Local Similarity   85.1%;  Pred. No. 9.9e-44;
  Matches   97;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          3 SGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSLK 62
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Db          1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60

Qy         63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGTLVTVSS 114
              ||||:||||||| |||:|||||||||||||||  |  | :| ||||| |||||
Db         61 SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDSGDYYGIDVWGQGTTVTVSS 114


RESULT 4
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-39

  Query Match             81.8%;  Score 502.5;  DB 4;  Length 119;
  Best Local Similarity   85.3%;  Pred. No. 2.3e-43;
  Matches   99;  Conservative    6;  Mismatches    6;  Indels    5;  Gaps    3;

Qy          2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYWSWIRQPPGKGLEWIGYIYHSGNTYYNPSL 61
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